

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 18, 2005, 12:39:38 ; Search time 44 Seconds
(without alignments)
478.897 Million cell updates/sec

Title: US-10-733-288A-4

Perfect score: 1140

Sequence: 1 IVGRRRPHAWPFMVSLQ.....PDAPVAFQFVNWDSIIQR 219

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1133	99.4	267	1	ELHUL
2	868.5	76.2	265	2	leukocyte elastase
3	637.5	55.9	256	1	PRHU3
4	480	42.1	231	1	TRHUZ
5	428	37.5	219	1	TRPGAZ
6	379	33.2	266	1	ELPG
7	366	32.1	266	1	ELRT1
8	364	31.9	258	4	S70439
9	364	31.9	267	4	A56615
10	344.5	30.2	261	2	S40162
11	343.5	30.1	282	1	A13172
12	341	29.9	258	2	I56220
13	340.5	29.9	226	2	S69370
14	338.5	29.7	255	2	A27122
15	338.5	29.7	263	1	I55608
16	337	29.6	244	2	A34910
17	336.5	29.5	259	1	WMMS28
18	336.5	29.5	269	2	A56823
19	335	29.4	246	1	DBHU
20	332.5	29.2	269	2	B26823
21	332.5	29.2	271	1	ELRT2
22	331.5	29.1	257	2	B45061
23	331.5	29.1	260	2	A45061
24	328.5	28.8	249	2	A55634
25	327.5	28.7	271	2	A25528
26	326.5	28.6	265	2	T10495
27	325	28.5	236	2	A28566
28	325	28.5	244	2	A46721
29	322.5	28.3	226	1	bradyruin (EC 3.4

RESULT 1

ELHUL

leukocyte elastase (EC 3.4.21.37) precursor [validated] - human
N;Alternate names: inflammatory serine proteinase; medullasin; neutrophil elastase
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1990 #sequence revision 30-Jun-1990 #text change 09-Jul-2004
C;Accession: A31976; S04954; S06241; A27064; S00631; A28370; A34570; A05293; A25907; S14;
R;Takahashi, H.; Nukiwa, T.; Yoshimura, K.; Quick, C.D.; States, D.J.; Holmes, M.D.; Whar
J. Biol. Chem. 263, 14739-14747, 1988

A;Title: Structure of the human neutrophil elastase gene.

A;Reference number: A31976; MUID:89008342; PMID:2902087

A;Accession: A31976

A;Molecule type: DNA

A;Residues: 1-267 <TAK>

A;Cross-references: UNIPROT:P08246; GB:M20203; GB:J04032; NID:g189147; PIDN:AAA36359.1; I

R;Farley, D.; Travis, J.; Salvesen, G.

Biol. Chem. Hoppe-Seyler 370, 737-744, 1989

A;Title: The human neutrophil elastase gene. Analysis of the nucleotide sequence reveals

A;Reference number: S04954; MUID:89374820; PMID:2775493

A;Accession: S04954

A;Status: not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-267 <FAR>

R;Nakamura, H.; Okano, K.; Aoki, Y.; Shimizu, H.; Naruto, M.

Nucleic Acids Res. 15, 9601-9602, 1987

A;Title: Nucleotide sequence of human bone marrow serine protease (medullasin) gene.

A;Reference number: S06241; MUID:88067782; PMID:3479752

A;Accession: S06241

A;Status: preliminary; translation not shown

A;Molecule type: DNA

A;Residues: 1-267 <NAK>

A;Cross-references: EMBL:X00477; NID:g34529; PIDN:CAA68537.1; PID:g296665

R;Okano, K.; Aoki, Y.; Sakurai, T.; Kajitani, M.; Kanai, S.; Shimizu, T.; Shimizu, H.; Ne

J. Biochem. 102, 13-16, 1987

A;Title: Molecular cloning of complementary DNA for human medullasin: an inflammatory se

A;Reference number: A27064; MUID:88032918; PMID:2822677

A;Accession: A27064

A;Molecule type: mRNA

A;Residues: 30-267 <OKA>

A;Cross-references: EMBL:X05875; NID:g34532; PIDN:CAA29300.1; PID:g1335212

A;Note: part of this sequence, including the amino end of the mature protein, was confir

R;Farley, D.; Salvesen, G.; Travis, J.

Biol. Chem. Hoppe-Seyler 369(Suppl.), 3-7, 1988

A;Title: Molecular cloning of human neutrophil elastase.

A;Reference number: S00631; MUID:89076526; PMID:2462434

A;Accession: S00631

A;Molecule type: mRNA

A;Residues: 123-267 <FA2>

A;Cross-references: GB:M27783; NID:g182055; PIDN:AAA35792.1; PID:g182056

A;Note: the authors translated the codon TTC for residue 218 as Pro

R;Takahashi, H.; Nukiwa, T.; Basset, P.; Crystal, R.G.

J. Biol. Chem. 263, 2543-2547, 1988

Db	210 GLIHGIASFVRGGCAGSLYPDAPFAPVAQFVNWIDSIQR 248	
RESULT 2		
148679	neutrophil elastase - mouse	
C:Species:	Mus musculus (house mouse)	
C:Date:	02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004	
C:Accession:	I48679	
R:Nuchprayoon, I.;	Meyers, S.; Scott, L.M.; Suzow, J.; Hiebert, S.; Friedman, A.D.	
Mol. Cell. Biol.	14, 5558-5568, 1994	
A:Title:	PEBP2/CBF, the murine homolog of the human myeloid AML1 and PEBP2 beta/CBF beta	
16.		
A:Reference number:	I48679; MUID:94309676; PMID:8035830	
A:Accession:	I48679	
A:Status:	preliminary; translated from GB/EMBL/DBJ	
A:Molecule type:	DNA	
A:Residues:	1-265 <RES>	
A:Cross-references:	UNIPROT:Q61515; EMBL:U04962; NID:9452556; PIDN:AAB60670.1; PID:945255	
C:Genetics:		
A:Introns:	22/1; 74/2; 121/3; 199/3	
C:Superfamily:	trypsin; trypsin homology	
F:29-242/Domain:	trypsin homology <TRY>	
Query Match	76.2%; Score 868.5; DB 2; Length 265;	
Best Local Similarity	75.9%; Pred. No. 1.4e-72;	
Matches	167; Conservative 19; Mismatches 33; Indels 1; Gaps 1;	
QY	1 IVGGRAPHPAPFVMSIQLRGHFCGATLIAPNFVMSAAHCVANVAVRVVLGAHNL 60	
Db	29 IVGGRAPHPAPFVMSIQLRGHFCGATLIAPNFVMSAAHCVANVAVRVVLGAHNL 88	
QY	61 SRRETRQVAVQRIFFENGTDVNLNDIVILQNGSATINANVOAQLPAQGRRLNGV 120	
Db	89 REQERTQTFVQGIFFENGTDVNLNDIVILQNGSATINANVOAQLPAQGRRLNGV 148	
QY	121 QCLAMGWLGNRGIAVQLQELNVTVVTSLC-RRSNVCTLVGRQAGVCFGDSGSPVLC 179	
Db	149 PCLAMGWSGLGNRFPSPVQLQELNVTVVTCPRRVNCTLVPRQAGICFGDSGSPVLC 208	
QY	180 NGLIHGIASFVRGGCAGSLYPDAPFAPVAQFVNWIDSIQR 219	
Db	209 NNLVQGISFIRGGCGSLYPDAPFAPVGEFVDWINSIIR 248	
RESULT 3		
PRHU3		
Proteinase 3 (EC 3.4.21.-)	precursor [validated] - human	
N;Alternate names:	AGP7; C-ANCA antigen; neutrophil proteinase 4; p29; Wegener's granuloma	
N;Contains:	myeloblastin	
C:Species:	Homo sapiens (man)	
C:Date:	31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004	
C:Accession:	A45080; B46268; A43983; JH0331; A33751; S11091; A61176; A60148; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A43982; A	

A;Reference number: A43983; MUID:92021028; PMID:1681549
A;Accession: A43983
A;Molecule type: mRNA
A;Residues: 1-69,'P',71-256 <LA2>
A;Cross-references: GB:M75154; NID:g187398; PIDN:AAA59558.1; PID:g187399
R;Campanelli, D.; Melchior, M.; Fu, Y.; Nakata, M.; Shuman, H.; Nathan, C.; Gabay, J.E.
J. Exp. Med. 172, 1709-1715, 1990
A;Title: Cloning of cDNA for proteinase 3: a serine protease, antibiotic, and autoantigen
A;Reference number: JH0331; MUID:91079774; PMID:2258701
A;Accession: JH0331
A;Molecule type: mRNA
A;Residues: 'R',3-118,'V',120-134,'AT',137-254,'P' <CAM>
A;Cross-references: GB:X55668; NID:g35687; PIDN:CAA39203.1; PID:g1335280
A;Note: Part of this sequence, including the amino end of the mature protein, was confirmed by Borjes, D.; Raynal, M.C.; Solomon, D.H.; Darzykiewicz, Z.; Cayre, Y.E.
Cell 59, 959-968, 1989
A;Title: Down-regulation of a serine protease, myeloblastin, causes growth arrest and differentiation of human myeloid leukemia cell lines
A;Reference number: A33751; MUID:90090622; PMID:2598267
A;Accession: A33751
A;Molecule type: mRNA
A;Residues: 42-256 <BOR>
A;Cross-references: GB:M29142; NID:g188983; PIDN:AAA36342.1; PID:g188984
A;Note: The authors translated the codon GGG for residue 49 as Glu, GGC for residue 52 as Gly, and GGC for residue 53 as Glu.
R;Jenne, D.E.; Tschopp, J.; Luedemann, J.; Utecht, B.; Gross, W.L.
Nature 346, 520, 1990
A;Title: Wegener's autoantigen decoded.
A;Reference number: S11091; MUID:90332035; PMID:2377228
A;Accession: S11091
A;Molecule type: mRNA
A;Residues: 20-56 <JEN>
R;Musette, P.; Labbaye, C.; Dorner, M.H.; Cayre, Y.E.; Casanova, J.L.; Kourilsky, P.
Blood 77, 1398-1399, 1991
A;Title: Wegener's autoantigen and leukemia.
A;Reference number: A61176; MUID:91159650; PMID:2001463
A;Accession: A61176
A;Molecule type: mRNA
A;Residues: 1-42 <MUS>
R;Cross-references: EMBL:X56606; NID:g35189; PIDN:CAA39943.1; PID:g35190
R;Goldschmeding, R.; Dolman, K.M.; Van Den Ende, M.E.; Van Der Meer-Gerritsen, C.H.; Son
APMIS Suppl. 19, 26-27, 1990
A;Title: The relation of 29 kD C-ANCA antigen to proteinase 3.
A;Reference number: A60148; MUID:91136884; PMID:2285532
A;Accession: A60148
A;Molecule type: protein
A;Residues: 28-48 <COL>
R;Rao, N.V.; Wehner, N.G.; Marshall, B.C.; Gray, W.R.; Gray, B.H.; Hoidal, J.R.
J. Biol. Chem. 266, 9540-9548, 1991
A;Title: Characterization of proteinase-3 (PR-3), a neutrophil serine proteinase. Structural and functional properties of the active site
A;Reference number: A43982; MUID:91236723; PMID:2033050
A;Accession: A43982
A;Molecule type: protein
A;Residues: 28-61,'X',63,'D',65-67;228-244 <RAO>
R;Wilde, C.G.; Snable, J.L.; Griffith, J.E.; Scott, R.W.
J. Biol. Chem. 265, 2038-2041, 1990
A;Title: Characterization of two azurophilic granule proteases with active-site homology to proteinase 3
A;Reference number: A43981; MUID:90130450; PMID:2404977
A;Accession: A43981
A;Molecule type: protein
A;Residues: 28-45,'E',47;196-208,'X',210-215,'X',217-219 <WIL>
R;Gabay, J.E.; Scott, R.W.; Campanelli, D.; Griffith, J.; Wilde, C.; Marra, M.N.; Seeger
Proc. Natl. Acad. Sci. U.S.A. 86, 5610-5614, 1989
A;Title: Antibiotic proteins of human polymorphonuclear leukocytes.
A;Reference number: A33913; MUID:89315847; PMID:2501794
A;Accession: C33913
A;Molecule type: protein
A;Residues: 28-45,'E',47 <GAB>
R;Niles, J.L.; McCluskey, R.T.; Ahmad, M.F.; Arnaout, M.A.
Blood 74, 1888-1893, 1989
A;Title: Wegener's granulomatosis autoantigen is a novel neutrophil serine proteinase.
A;Reference number: A60481; MUID:90028708; PMID:2679910
A;Accession: A60481
A;Molecule type: protein
A;Residues: 28-36,'X',40-47 <NI2>

R;Ohlsson, K.; Linder, C.; Rosengren, M.
Biol. Chem. Hoppe-Seyler 371, 549-555, 1990
A;Title: Monoclonal antibodies specific for neutrophil proteinase 4. Production and use in the diagnosis of Wegener's granulomatosis
A;Reference number: S10605; MUID:91025622; PMID:2121162
A;Accession: S10605
A;Molecule type: protein
A;Residues: 28-52 <OHL>
R;Luedemann, J.; Utecht, B.; Gross, W.L.
J. Exp. Med. 171, 357-362, 1990
A;Title: Anti-neutrophil cytoplasm antibodies in Wegener's granulomatosis recognize an epitope on proteinase 3
A;Reference number: PLO230; MUID:90111630; PMID:1688612
A;Accession: PLO230
A;Molecule type: protein
A;Residues: 28-37,'I',39-40,'I',41-43 <LUJ>
C;Comment: This polymorphonuclear leukocyte serine protease from azurophilic granules described by Ohlsson, K.; Linder, C.; Rosengren, M.; Luedemann, J.; Utecht, B.; Gross, W.L.
C;Genetics:
A;Gene: GDB:PRTN3
A;Cross-references: GDB:126876; OMIM:177020
A;Map position: 19p13.3-19p13.3
A;Introns: 21/1; 76/2; 123/3; 200/3
C;Superfamily: trypsin; trypsin homology
C;Keywords: glycoprotein; hydrolase; polymorphonuclear leukocyte; serine proteinase
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-27/Domain: propeptide #status predicted <PRO>
F;28-256/Product: proteinase 3 #status experimental <MAT>
F;28-243/Domain: trypsin homology <TRY>
F;56-72;152-209;182-188;199-224/Disulfide bonds: #status predicted
F;71,118,203/Active site: His, Asp, Ser #status predicted
F;129,174/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 55.9%; Score 637.5; DB 1; Length 256;
Best Local Similarity 54.5%; Pred. NO. 2.6e-51;
Matches 121; Conservative 40; Mismatches 58; Indels 3; Gaps 1;
QY 1 IVGRRARPHAMPVMSLOLR---GGHFCGATLIAPNFVMSAAHCVANNVRAVRVVLGA 57
Db 28 IVGGHEAQPSPYMASLQMRGNPGSHFCGGLIHPSFVLTAACHURDIPQRULNVVLGA 87
QY 58 HNLSRREPQVAFQVQIFENGTDVPMNLNDIVILQNGSATINANVQVLAQAQRRRLG 117
Db 88 HNVRTQEPQHFSAQVFLNNYDAENKLDILLQLSSPANLSASVTSVQLPQQQPVP 147
QY 118 NGVQCLAMGWLGNRGIASVQLBELNVTVVTSLSRRSNVCTLVGRQAGVCFGDSGSPL 177
Db 148 HGTQCLAMGWRGVADPPAQVLQELNVTVVTFPCRPHNICTFVPRKAGICFGDSGGPL 207
QY 178 VCNGLIHGTASVRCGSCAGLYPDAPAPVAFQVFNWIDSIIQR 219
Db 208 ICDGIQGDISFVWGCATRLFPDFTRVALYVDWIRSLRR 249
RESULT 4
TRUAZ
azurocidin precursor [validated] - human
N;Alternate names: cationic antimicrobial protein CAP37; heparin-binding protein; neutrophil proteinase 3
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence revision 30-Sep-1993 #text change 09-Jul-2004
R;Accession: A46268; A46455; S16450; S18851; S15445; S14738; B33913; A60708; B436
R;Zimmer, M.; Medcalf, R.L.; Fink, T.M.; Mattmann, C.; Lichter, P.; Jenne, D.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 8215-8219, 1992
A;Title: Three human elastase-like genes coordinately expressed in the myelomonocyte lineage
A;Reference number: A46268; MUID:92390417; PMID:1518849
A;Accession: A46268
A;Molecule type: DNA
A;Residues: 1-251 <ZIM>
A;Cross-references: UNIPROT:P20160; GB:M96326; NID:g179301; PIDN:AA59353.1; PID:g179302
A;Note: Sequence extracted from NCBI backbone (NCBIN:112883, NCBIN:112891, NCBIN:112893, NCBIN:112895, NCBIN:112897, NCBIN:112899, NCBIN:112901, NCBIN:112903, NCBIN:112905, NCBIN:112907, NCBIN:112909, NCBIN:112911, NCBIN:112913, NCBIN:112915, NCBIN:112917, NCBIN:112919, NCBIN:112921, NCBIN:112923, NCBIN:112925, NCBIN:112927, NCBIN:112929, NCBIN:112931, NCBIN:112933, NCBIN:112935, NCBIN:112937, NCBIN:112939, NCBIN:112941, NCBIN:112943, NCBIN:112945, NCBIN:112947, NCBIN:112949, NCBIN:112951, NCBIN:112953, NCBIN:112955, NCBIN:112957, NCBIN:112959, NCBIN:112961, NCBIN:112963, NCBIN:112965, NCBIN:112967, NCBIN:112969, NCBIN:112971, NCBIN:112973, NCBIN:112975, NCBIN:112977, NCBIN:112979, NCBIN:112981, NCBIN:112983, NCBIN:112985, NCBIN:112987, NCBIN:112989, NCBIN:112991, NCBIN:112993, NCBIN:112995, NCBIN:112997, NCBIN:112999, NCBIN:113001, NCBIN:113003, NCBIN:113005, NCBIN:113007, NCBIN:113009, NCBIN:113011, NCBIN:113013, NCBIN:113015, NCBIN:113017, NCBIN:113019, NCBIN:113021, NCBIN:113023, NCBIN:113025, NCBIN:113027, NCBIN:113029, NCBIN:113031, NCBIN:113033, NCBIN:113035, NCBIN:113037, NCBIN:113039, NCBIN:113041, NCBIN:113043, NCBIN:113045, NCBIN:113047, NCBIN:113049, NCBIN:113051, NCBIN:113053, NCBIN:113055, NCBIN:113057, NCBIN:113059, NCBIN:113061, NCBIN:113063, NCBIN:113065, NCBIN:113067, NCBIN:113069, NCBIN:113071, NCBIN:113073, NCBIN:113075, NCBIN:113077, NCBIN:113079, NCBIN:113081, NCBIN:113083, NCBIN:113085, NCBIN:113087, NCBIN:113089, NCBIN:113091, NCBIN:113093, NCBIN:113095, NCBIN:113097, NCBIN:113099, NCBIN:113101, NCBIN:113103, NCBIN:113105, NCBIN:113107, NCBIN:113109, NCBIN:113111, NCBIN:113113, NCBIN:113115, NCBIN:113117, NCBIN:113119, NCBIN:113121, NCBIN:113123, NCBIN:113125, NCBIN:113127, NCBIN:113129, NCBIN:113131, NCBIN:113133, NCBIN:113135, NCBIN:113137, NCBIN:113139, NCBIN:113141, NCBIN:113143, NCBIN:113145, NCBIN:113147, NCBIN:113149, NCBIN:113151, NCBIN:113153, NCBIN:113155, NCBIN:113157, NCBIN:113159, NCBIN:113161, NCBIN:113163, NCBIN:113165, NCBIN:113167, NCBIN:113169, NCBIN:113171, NCBIN:113173, NCBIN:113175, NCBIN:113177, NCBIN:113179, NCBIN:113181, NCBIN:113183, NCBIN:113185, NCBIN:113187, NCBIN:113189, NCBIN:113191, NCBIN:113193, NCBIN:113195, NCBIN:113197, NCBIN:113199, NCBIN:113201, NCBIN:113203, NCBIN:113205, NCBIN:113207, NCBIN:113209, NCBIN:113211, NCBIN:113213, NCBIN:113215, NCBIN:113217, NCBIN:113219, NCBIN:113221, NCBIN:113223, NCBIN:113225, NCBIN:113227, NCBIN:113229, NCBIN:113231, NCBIN:113233, NCBIN:113235, NCBIN:113237, NCBIN:113239, NCBIN:113241, NCBIN:113243, NCBIN:113245, NCBIN:113247, NCBIN:113249, NCBIN:113251, NCBIN:113253, NCBIN:113255, NCBIN:113257, NCBIN:113259, NCBIN:113261, NCBIN:113263, NCBIN:113265, NCBIN:113267, NCBIN:113269, NCBIN:113271, NCBIN:113273, NCBIN:113275, NCBIN:113277, NCBIN:113279, NCBIN:113281, NCBIN:113283, NCBIN:113285, NCBIN:113287, NCBIN:113289, NCBIN:113291, NCBIN:113293, NCBIN:113295, NCBIN:113297, NCBIN:113299, NCBIN:113301, NCBIN:113303, NCBIN:113305, NCBIN:113307, NCBIN:113309, NCBIN:113311, NCBIN:113313, NCBIN:113315, NCBIN:113317, NCBIN:113319, NCBIN:113321, NCBIN:113323, NCBIN:113325, NCBIN:113327, NCBIN:113329, NCBIN:113331, NCBIN:113333, NCBIN:113335, NCBIN:113337, NCBIN:113339, NCBIN:113341, NCBIN:113343, NCBIN:113345, NCBIN:113347, NCBIN:113349, NCBIN:113351, NCBIN:113353, NCBIN:113355, NCBIN:113357, NCBIN:113359, NCBIN:113361, NCBIN:113363, NCBIN:113365, NCBIN:113367, NCBIN:113369, NCBIN:113371, NCBIN:113373, NCBIN:113375, NCBIN:113377, NCBIN:113379, NCBIN:113381, NCBIN:113383, NCBIN:113385, NCBIN:113387, NCBIN:113389, NCBIN:113391, NCBIN:113393, NCBIN:113395, NCBIN:113397, NCBIN:113399, NCBIN:113401, NCBIN:113403, NCBIN:113405, NCBIN:113407, NCBIN:113409, NCBIN:113411, NCBIN:113413, NCBIN:113415, NCBIN:113417, NCBIN:113419, NCBIN:113421, NCBIN:113423, NCBIN:113425, NCBIN:113427, NCBIN:113429, NCBIN:113431, NCBIN:113433, NCBIN:113435, NCBIN:113437, NCBIN:113439, NCBIN:113441, NCBIN:113443, NCBIN:113445, NCBIN:113447, NCBIN:113449, NCBIN:113451, NCBIN:113453, NCBIN:113455, NCBIN:113457, NCBIN:113459, NCBIN:113461, NCBIN:113463, NCBIN:113465, NCBIN:113467, NCBIN:113469, NCBIN:113471, NCBIN:113473, NCBIN:113475, NCBIN:113477, NCBIN:113479, NCBIN:113481, NCBIN:113483, NCBIN:113485, NCBIN:113487, NCBIN:113489, NCBIN:113491, NCBIN:113493, NCBIN:113495, NCBIN:113497, NCBIN:113499, NCBIN:113501, NCBIN:113503, NCBIN:113505, NCBIN:113507, NCBIN:113509, NCBIN:113511, NCBIN:113513, NCBIN:113515, NCBIN:113517, NCBIN:113519, NCBIN:113521, NCBIN:113523, NCBIN:113525, NCBIN:113527, NCBIN:113529, NCBIN:113531, NCBIN:113533, NCBIN:113535, NCBIN:113537, NCBIN:113539, NCBIN:113541, NCBIN:113543, NCBIN:113545, NCBIN:113547, NCBIN:113549, NCBIN:113551, NCBIN:113553, NCBIN:113555, NCBIN:113557, NCBIN:113559, NCBIN:113561, NCBIN:113563, NCBIN:113565, NCBIN:113567, NCBIN:113569, NCBIN:113571, NCBIN:113573, NCBIN:113575, NCBIN:113577, NCBIN:113579, NCBIN:113581, NCBIN:113583, NCBIN:113585, NCBIN:113587, NCBIN:113589, NCBIN:113591, NCBIN:113593, NCBIN:113595, NCBIN:113597, NCBIN:113599, NCBIN:113601, NCBIN:113603, NCBIN:113605, NCBIN:113607, NCBIN:113609, NCBIN:113611, NCBIN:113613, NCBIN:113615, NCBIN:113617, NCBIN:113619, NCBIN:113621, NCBIN:113623, NCBIN:113625, NCBIN:113627, NCBIN:113629, NCBIN:113631, NCBIN:113633, NCBIN:113635, NCBIN:113637, NCBIN:113639, NCBIN:113641, NCBIN:113643, NCBIN:113645, NCBIN:113647, NCBIN:113649, NCBIN:113651, NCBIN:113653, NCBIN:113655, NCBIN:113657, NCBIN:113659, NCBIN:113661, NCBIN:113663, NCBIN:113665, NCBIN:113667, NCBIN:113669, NCBIN:113671, NCBIN:113673, NCBIN:113675, NCBIN:113677, NCBIN:113679, NCBIN:113681, NCBIN:113683, NCBIN:113685, NCBIN:113687, NCBIN:113689, NCBIN:113691, NCBIN:113693, NCBIN:113695, NCBIN:113697, NCBIN:113699, NCBIN:113701, NCBIN:113703, NCBIN:113705, NCBIN:113707, NCBIN:113709, NCBIN:113711, NCBIN:113713, NCBIN:113715, NCBIN:113717, NCBIN:113719, NCBIN:113721, NCBIN:113723, NCBIN:113725, NCBIN:113727, NCBIN:113729, NCBIN:113731, NCBIN:113733, NCBIN:113735, NCBIN:113737, NCBIN:113739, NCBIN:113741, NCBIN:113743, NCBIN:113745, NCBIN:113747, NCBIN:113749, NCBIN:113751, NCBIN:113753, NCBIN:113755, NCBIN:113757, NCBIN:113759, NCBIN:113761, NCBIN:113763, NCBIN:113765, NCBIN:113767, NCBIN:113769, NCBIN:113771, NCBIN:113773, NCBIN:113775, NCBIN:113777, NCBIN:113779, NCBIN:113781, NCBIN:113783, NCBIN:113785, NCBIN:113787, NCBIN:113789, NCBIN:113791, NCBIN:113793, NCBIN:113795, NCBIN:113797, NCBIN:113799, NCBIN:113801, NCBIN:113803, NCBIN:113805, NCBIN:113807, NCBIN:113809, NCBIN:113811, NCBIN:113813, NCBIN:113815, NCBIN:113817, NCBIN:113819, NCBIN:113821, NCBIN:113823, NCBIN:113825, NCBIN:113827, NCBIN:113829, NCBIN:113831, NCBIN:113833, NCBIN:113835, NCBIN:113837, NCBIN:113839, NCBIN:113841, NCBIN:113843, NCBIN:113845, NCBIN:113847, NCBIN:113849, NCBIN:113851, NCBIN:113853, NCBIN:113855, NCBIN:113857, NCBIN:113859, NCBIN:113861, NCBIN:113863, NCBIN:113865, NCBIN:113867, NCBIN:113869, NCBIN:113871, NCBIN:113873, NCBIN:113875, NCBIN:113877, NCBIN:113879, NCBIN:113881, NCBIN:113883, NCBIN:113885, NCBIN:113887, NCBIN:113889, NCBIN:113891, NCBIN:113893, NCBIN:113895, NCBIN:113897, NCBIN:113899, NCBIN:113901, NCBIN:113903, NCBIN:113905, NCBIN:113907, NCBIN:113909, NCBIN:113911, NCBIN:113913, NCBIN:113915, NCBIN:113917, NCBIN:113919, NCBIN:113921, NCBIN:113923, NCBIN:113925, NCBIN:113927, NCBIN:113929, NCBIN:113931, NCBIN:113933, NCBIN:113935, NCBIN:113937, NCBIN:113939, NCBIN:113941, NCBIN:113943, NCBIN:113945, NCBIN:113947, NCBIN:113949, NCBIN:113951, NCBIN:113953, NCBIN:113955, NCBIN:113957, NCBIN:113959, NCBIN:113961, NCBIN:113963, NCBIN:113965, NCBIN:113967, NCBIN:113969, NCBIN:113971, NCBIN:113973, NCBIN:113975, NCBIN:113977, NCBIN:113979, NCBIN:113981, NCBIN:113983, NCBIN:113985, NCBIN:113987, NCBIN:113989, NCBIN:113991, NCBIN:113993, NCBIN:113995, NCBIN:113997, NCBIN:113999, NCBIN:114001, NCBIN:114003, NCBIN:114005, NCBIN:114007, NCBIN:114009, NCBIN:114011, NCBIN:114013, NCBIN:114015, NCBIN:114017, NCBIN:114019, NCBIN:114021, NCBIN:114023, NCBIN:114025, NCBIN:114027, NCBIN:114029, NCBIN:114031, NCBIN:114033, NCBIN:114035, NCBIN:114037, NCBIN:114039, NCBIN:114041, NCBIN:114043, NCBIN:114045, NCBIN:114047, NCBIN:114049, NCBIN:114051, NCBIN:114053, NCBIN:114055, NCBIN:114057, NCBIN:114059, NCBIN:114061, NCBIN:114063, NCBIN:114065, NCBIN:114067, NCBIN:114069, NCBIN:114071, NCBIN:114073, NCBIN:114075, NCBIN:114077, NCBIN:114079, NCBIN:114081, NCBIN:114083, NCBIN:114085, NCBIN:114087, NCBIN:114089, NCBIN:114091, NCBIN:114093, NCBIN:114095, NCBIN:114097, NCBIN:114099, NCBIN:114101, NCBIN:114103, NCBIN:114105, NCBIN:114107, NCBIN:114109, NCBIN:114111, NCBIN:114113, NCBIN:114115, NCBIN:114117, NCBIN:114119, NCBIN:114121, NCBIN:114123, NCBIN:114125, NCBIN:114127, NCBIN:114129, NCBIN:114131, NCBIN:114133, NCBIN:114135, NCBIN:114137, NCBIN:114139, NCBIN:114141, NCBIN:114143, NCBIN:114145, NCBIN:114147, NCBIN:114149, NCBIN:114151, NCBIN:114153, NCBIN:114155, NCBIN:114157, NCBIN:114159, NCBIN:114161, NCBIN:114163, NCBIN:114165, NCBIN:114167, NCBIN:114169, NCBIN:114171, NCBIN:114173, NCBIN:114175, NCBIN:114177, NCBIN:114179, NCBIN:114181, NCBIN:114183, NCBIN:114185, NCBIN:114187, NCBIN:114189, NCBIN:114191, NCBIN:114193, NCBIN:114195, NCBIN:114197, NCBIN:114199, NCBIN:114201, NCBIN:114203, NCBIN:114205, NCBIN:114207, NCBIN:114209, NCBIN:114211, NCBIN:114213, NCBIN:114215, NCBIN:114217, NCBIN:114219, NCBIN:114221, NCBIN:114223, NCBIN:114225, NCBIN:114227, NCBIN:114229, NCBIN:114231, NCBIN:114233, NCBIN:114235, NCBIN:114237, NCBIN:114239, NCBIN:114241, NCBIN:114243, NCBIN:114245, NCBIN:114247, NCBIN:114249, NCBIN:114251, NCBIN:114253, NCBIN:114255, NCBIN:114257, NCBIN:114259, NCBIN:114261, NCBIN:114263, NCBIN:114265, NCBIN:114267, NCBIN:114269, NCBIN:114271, NCBIN:114273, NCBIN:114275, NCBIN:114277, NCBIN:114279, NCBIN:114281, NCBIN:114283, NCBIN:114285, NCBIN:114287, NCBIN:114289, NCBIN:114291, NCBIN:114293, NCBIN:114295, NCBIN:114297, NCBIN:114299, NCBIN:114301, NCBIN:114303, NCBIN:114305, NCBIN:114307, NCBIN:114309, NCBIN:114311, NCBIN:114313, NCBIN:114315, NCBIN:114317, NCBIN:114319, NCBIN:114321, NCBIN:114323, NCBIN:114325, NCBIN:114327, NCBIN:114329, NCBIN:114331, NCBIN:114333, NCBIN:114335, NCBIN:114337, NCBIN:114339, NCBIN:114341, NCBIN:114343, NCBIN:114345, NCBIN:114347, NCBIN:114349, NCBIN:114351, NCBIN:114353, NCBIN:114355, NCBIN:114357, NCBIN:114359, NCBIN:114361, NCBIN:114363, NCBIN:114365, NCBIN:114367, NCBIN:114369, NCBIN:114371, NCBIN:114373, NCBIN:114375, NCBIN:114377, NCBIN:114379, NCBIN:114381, NCBIN:114383, NCBIN:114385, NCBIN:114387, NCBIN:114389, NCBIN:114391, NCBIN:114393, NCBIN:114395, NCBIN:114397, NCBIN:114399, NCBIN:114401, NCBIN:114403, NCBIN:114405, NCBIN:114407, NCBIN:114409, NCBIN:114411, NCBIN:114413, NCBIN:114415, NCBIN:114417, NCBIN:114419, NCBIN:114421, NCBIN:114423, NCBIN:114425, NCBIN:114427, NCBIN:114429, NCBIN:114431, NCBIN:114433, NCBIN:114435, NCBIN:114437, NCBIN:114439, NCBIN:114441, NCBIN:114443, NCBIN:114445, NCBIN:114447, NCBIN:114449, NCBIN:114451, NCBIN:114453, NCBIN:114455, NCBIN:114457, NCBIN:114459, NCBIN:114461, NCBIN:114463, NCBIN:114465, NCBIN:114467, NCBIN:114469, NCBIN:114471, NCBIN:114473, NCBIN:114475, NCBIN:114477, NCBIN:114479, NCBIN:114481, NCBIN:114483, NCBIN:114485, NCBIN:114487, NCBIN:114489, NCBIN:114491, NCBIN:114493, NCBIN:114495, NCBIN:114497, NCBIN:114499, NCBIN:114501, NCBIN:114503, NCBIN:114505, NCBIN:114507, NCBIN:114509, NCBIN:114511, NCBIN:114513, NCBIN:114515, NCBIN:114517, NCBIN:114519, NCBIN:114521, NCBIN:114523, NCBIN:114525, NCBIN:114527, NCBIN:114529, NCBIN:114531, NCBIN:114533, NCBIN:114535, NCBIN:114537, NCBIN:114539, NCBIN:114541, NCBIN:114543, NCBIN:114545, NCBIN:114547, NCBIN:114549, NCBIN:114551, NCBIN:114553, NCBIN:114555, NCBIN:114557, NCBIN:114559, NCBIN:114561, NCBIN:114563, NCBIN:114565, NCBIN:114567, NCBIN:114569, NCBIN:114571, NCBIN:114573, NCBIN:114575, NCBIN:114577, NCBIN:114579, NCBIN:114581, NCBIN:114583, NCBIN:114585, NCBIN:114587, NCBIN:114589, NCBIN:114591, NCBIN:114593, NCBIN:114595, NCBIN:114597, NCBIN:114599, NCBIN:114601, NCBIN:114603, NCBIN:114605, NCBIN:114607, NCBIN:114609, NCBIN:114611, NCBIN:114613, NCBIN:114615, NCBIN:114617, NCBIN:114619, NCBIN:114621, NCBIN:114623, NCBIN:114625, NCBIN:114627, NCBIN:114629, NCBIN:114631, NCBIN:114633, NCBIN:114635, NCBIN:114637, NCBIN:114639, NCBIN:114641, NCBIN:

R;Wilde, C.G.; Snable, J.L.; Griffith, J.E.; Scott, R.W.
J. Biol. Chem. 285, 2038-2041, 1990
A;Title: Characterization of two azurophil granule proteases with active-site homology to
A;Reference number: A43981; MUID:90130450; PMID:2404977
A;Accession: B43981
A;Molecule type: protein
A;Residues: 27-35 'H', 37-46;194-217 <WIL>
R;Pereira, H.A.; Spitznagel, J.K.; Pohl, J.; Wilson, D.E.; Morgan, J.; Palings, I.; Larric
Life Sci. 46, 189-196, 1990
A;Title: CAP 37, a 37 kD human neutrophil granule cationic protein shares homology with i
A;Reference number: PH0081; MUID:90157837; PMID:2406527
A;Accession: PH0081
A;Molecule type: protein
A;Residues: 27-67 <PE2>
A;Experimental source: polymorphonuclear leukocyte
C;Comment: This protein is homologous to serine proteinases but lacks proteolytic activit
icrobial activity against a number of gram-negative bacteria.
C;Genetics:
A;Gene: GDB:AZU1
A;Cross-references: GDB:135033; OMIM:162815
A;Map position: 19p13.3-19p13.3
A;Introns: 20/1; 72/2; 150/3; 198/3
C;Superfamily: trypsin; trypsin homology
C;Keywords: glycoprotein; inflammation
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-26/Domain: amino-terminal propeptide #status predicted <PRO>
F;27-248/Product: azurocidin #status experimental <MAT>
F;27-239/Domain: trypsin homology <TRY>
F;27,115,201/Region: defective catalytic triad
F;249-251/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;52-68/Disulfide bonds: #status experimental
F;126,140,171/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;149-207,180-186,197-222/Disulfide bonds: #status predicted

Query Match 42.1%; Score 480; DB 1; Length 251;
Best Local Similarity 45.2%; Pred. No. 8.6e-37;
Matches 99; Conservative 35; Mismatches 81; Indels 4; Gaps 3;

QY 1 IVGGRARPHAWPFMVSLQLRGHFCGATLIAPNFVMSAAHCVANVNRVAVVGLGAHNL 60
DB 27 IVGGRKARPRQFPFLASIQNGRHFCCGALIHARFVMTAASCFSQNPQGVSTVVLGAYDL 86
QY 61 SRRE-PTROVFAVQRIENGTDPNLLNDIVILQNGSATINANVOVAQLPAQGRRLGNG 119
DB 87 RRRERQSRQTSFTSISSSENGYDPPQNLNDIMLLQDLREANLTSVTILPLPLQNAIVEAG 146
QY 120 VQCLAWGMLGNRGCIASVLQBLNTVW-TSLCRSRNVCTLVVRGQAGVCFGDSGSLV 178
DB 147 TRCQVAGMSQSGRLSPFRFVNTVTPDQCRPNVCTGVLTTRGGICNGDGGTPLV 206
QY 179 CNGLIHGIIASFVRGGCAGSLYDPAFPVQFVNWIDSII 217
DB 207 CEGLAGHVASFLGPGCGR--PDFFTRVALFRDWIDGVL 243

RESULT 5
TREGAZ
azurocidin - pig
N;Alternate names: heparin-binding protein
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: S15393
R;Flodgaard, H.; Ostergaard, E.; Bayne, S.; Svendsen, A.; Thomsen, J.; Engels, M.; Wollm
Eur. J. Biochem. 197, 535-547, 1991
A;Title: Covalent structure of two novel neutrophil leucocyte-derived proteins of porci
A;Reference number: S15393; MUID:91224149; PMID:2026172
A;Accession: S15393
A;Molecule type: protein
A;Residues: 1-219 <FLO>
A;Cross-references: UNIPROT:P80015
R;Sorensen, H.H.; Thomsen, J.; Bayne, S.; Hojrup, P.; Roepstorff, P.
Biomed. Environ. Mass Spectrom. 19, 713-720, 1990


```
RESULT 8
S70439
pancreatic elastase I (allele HELI-16) probable splice form I - human
C:Species: Homo sapiens (man)
C>Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 28-Apr-2003
C:Accession: S70439
R:Kawashima, I.; Tani, T.; Mita-Honjo, K.; Shimoda-Takano, K.; Ohmine, T.; Furukawa, H.;
DNA Seq. 2, 303-312, 1992
A:Title: Genomic organization of the human homologue of the rat pancreatic elastase I
A:Reference number: A56615; MUID:92338395; PMID:1633328
A:Accession: S70439
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-258 <KAW>
A>Note: it is not known whether the gene is expressed
F:19-251/Domain: trypsin homology <TRY>

Query Match 31.9%; Score 364; DB 4; Length 258;
Best Local Similarity 38.3%; Pred. No. 4.4e-26;
Matches 92; Conservative 37; Mismatches 85; Indels 26; Gaps 9;

Qy 1 IVGRRARPHAWPFMVSLQLRG----HFCGATLIAPNFVMSAAHCVANVAVRVVLG 56
Db 19 VVGTEAGRNWPSQISLQVRSQGSWYHTCGGTLIRQNVWMTAAHCVD--YQKTRFVAVG 76

Qy 57 AHNLSRREPTROVFAVORIFEN---GTDPVNLLNDIVILQNGSATINANVOVQAQ 113
Db 77 DHNLSQNDQTEQVSVQKIVVHPYNSNDVAAGYDIALRLAQSVTLNSVQLGVLPQEG 136

Qy 114 RRLNGVQCLAMGWGLLGRNRIASVLQELNV--TVVTSLCRRSN-----VCTLVR 162
Db 137 AILANNSPCYITGWKTKTNGLAQTLOQAYLPSVDYVAICSSSSYWGSTVKTMTWCAGGD 196

Qy 163 GRQAGVCFDGSGLPVC--NG--LIHGIAFVRG--GCASGLYPDAFPAVQFVNWIDSII 217
Db 197 GVRSG-CQGDGGGLHCLVNGKYSLHGVTFSVSRGCVNSRKPTVFTFRVSAIYSWINNVI 255

RESULT 9
A56615
probable pancreatic elastase (EC 3.4.21.36) pseudogene - human
N:Alternate names: pancreatic elastase I homolog; pancreatic elastase I allele HELI-16,
C:Species: Homo sapiens (man)
C>Date: 11-Aug-1995 #sequence_revision 17-Aug-1995 #text_change 14-Aug-1998
C:Accession: A56615; S70440
R:Kawashima, I.; Tani, T.; Mita-Honjo, K.; Shimoda-Takano, K.; Ohmine, T.; Furukawa, H.;
DNA Seq. 2, 303-312, 1992
A:Title: Genomic organization of the human homologue of the rat pancreatic elastase I
A:Reference number: A56615; MUID:92338395; PMID:1633328
A:Accession: A56615
A:Molecule type: DNA
A:Residues: 1-267 <KAW>
A:Cross-references: EMBL:X62258; NID:931246; EMBL:X62258; GB:S40923; NID:931247; EMBL:X6
5; GB:S40856; NID:931251; EMBL:X62256; GB:S40857; NID:931252; EMBL:X62257; GB:S40859; NI
A>Note: sequence extracted from NCBI backbone (NCBIN:109315, NCBIN:109317, NCBIN:109319,
C:Comment: This apparently silent human homolog of pancreatic elastase I is a single-co
functional protein in some other tissue.
C:Genetics:
A:Gene: GDB:ELAL
A:Map position: 12
C:Keywords: hydrolase; pseudogene; serine proteinase

Query Match 31.9%; Score 364; DB 4; Length 267;
Best Local Similarity 38.3%; Pred. No. 4.6e-26;
Matches 92; Conservative 37; Mismatches 85; Indels 26; Gaps 9;

Qy 1 IVGRRARPHAWPFMVSLQLRG----HFCGATLIAPNFVMSAAHCVANVAVRVVLG 56
Db 28 VVGTEAGRNWPSQISLQVRSQGSWYHTCGGTLIRQNVWMTAAHCVD--YQKTRFVAVG 85

Qy 57 AHNLSRREPTROVFAVORIFEN---GTDPVNLLNDIVILQNGSATINANVOVQAQ 113
Db 86 DHNLSQNDQTEQVSVQKIVVHPYNSNDVAAGYDIALRLAQSVTLNSVQLGVLPQEG 145
```

```
Qy 114 RRLNGVQCLAMGWGLLGRNRIASVLQELNV--TVVTSLCRRSN-----VCTLVR 162
Db 146 AILANNSPCYITGWKTKTNGLAQTLOQAYLPSVDYVAICSSSSYWGSTVKTMTWCAGGD 205

Qy 163 GRQAGVCFDGSGLPVC--NG--LIHGIAFVRG--GCASGLYPDAFPAVQFVNWIDSII 217
Db 206 GVRSG-CQGDGGGLHCLVNGKYSLHGVTFSVSRGCVNSRKPTVFTFRVSAIYSWINNVI 264

RESULT 10
S40162
cathopsin G (EC 3.4.21.20) precursor - mouse
N:Alternate names: vimentin-specific proteinase
C:Species: Mus musculus (house mouse)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S40162; A48932; S23170
R:Kulmburg, P.; Baumruker, T.
A:Title: Molecular cloning, chromosomal location, and tissue-specific expression of the n
A:Reference number: A48932; MUID:93200524; PMID:8453108
A:Accession: S40162
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-261 <KUL>
A:Cross-references: UNIPROT:P28293; EMBL:X70057; NID:9437879; PIDN:CAAM9661.1; PID:943788
R:Heusel, J.W.; Scarpati, E.M.; Jenkins, N.A.; Gilbert, D.J.; Copeland, N.G.; Shapiro, S.
Blood 81, 1614-1623, 1993
A:Title: Molecular cloning, chromosomal location, and tissue-specific expression of the n
A:Reference number: A48932; MUID:93200524; PMID:8453108
A:Accession: S40162
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-261 <HEU>
A:Cross-references: GB:M96801; NID:G192383; PIDN:AAA37376.1; PID:G192384
A>Note: sequence extracted from NCBI backbone (NCBIN:127495, NCBI:P:127496)
R:Nakamura, N.; Tsuru, A.; Hirayoshi, K.; Nagata, K.
Eur. J. Biochem. 205, 947-954, 1992
A:Title: Purification and characterization of a vimentin-specific protease in mouse myelc
A:Reference number: S23170; MUID:92249339; PMID:1577012
A:Accession: S23170
A:Status: preliminary
A:Molecule type: protein
A:Residues: 21-23, 'X', 25-44, 'X', 46, 'X', 48, 'XXS', 52-54, 'XG', 57-59, 'P' <NAK>
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; serine proteinase
F:21-238/Domain: trypsin homology <TRY>
F:64,108,201/Active site: His, Asp, Ser #status predicted

Query Match 30.2%; Score 344.5; DB 2; Length 261;
Best Local Similarity 34.1%; Pred. No. 2.8e-24;
Matches 79; Conservative 47; Mismatches 85; Indels 21; Gaps 7;

Qy 1 IVGRRARPHAWPFMVSLQLR---GGHFCGATLIAPNFVMSAAHCVANVAVRVVLGA 57
Db 21 IIGREARPHSPYPMYAFLLIQSPEGLSACGGFLVRDFVLTAAHCLGS----SINTVLLGA 76

Qy 58 HNLSRREPTROVFAVORIFEN--GTDPVNLLNDIVILQNGSATINANVOVQAQ 116
Db 77 HNTQMRERTQQLITVLRAIRHPDYNFQNRNDIMLLQRRRRARRSGSVFVPAQASKL 136

Qy 117 GNGVQCLAMGWGLLGRNRIASVLQELNVTV--VTSLC-----RRSNVCTLVRGRQAG 167
Db 137 QPGLDLCTVAGKRVQSQRG--TNVLQEVQLRVQMDQMCANRFQFYNSTQICVGNPREKS 195

Qy 168 VCFDGSGLPVCNGLIHGIAFVRGCGASGLYPDAFPAVQFVNWIDSIIOR 219
Db 196 AFRGDSGGPLVCSNVAQGIYSY---GSNNNGNPPAVFTKIQSFMPWIKRTMRR 244

RESULT 11
A31372
granzyme A (EC 3.4.21.78) precursor [validated] - human
```

tryptase 2 - rat

RESULT 14
A27122
cathepsin G (EC 3.4.21.20) precursor - human
N/Alternate names: membrane-associated proteinase, U937 cell; neutrophil cathepsin G
C/Species: Homo sapiens (man)
C/Date: 05-Jun-1988 #sequence revision 05-Jun-1988 #text_change 09-Jul-2004
A/Accession: A32627; A46471; A37115; S44427; A90031; A94428; A05307
R/Hohn, P.A.; Popescu, N.C.; Hanson, R.D.; Salvesen, G.; Ley, T.J.
J. Biol. Chem. 264, 13412-13419, 1989
A/Title: Genomic organization and chromosomal localization of the human cathepsin G gene
A/Reference number: A32627; MUID:89340411; PMID:2569462
A/Accession: A32627
A/Molecule type: DNA
A/Residues: 1-255 <H>
A/Cross-references: UNIPROT:P08311; GB:J04990; NID:G179914; PIDN:AAA51919.1; PID:G179915
R/Salvesen, G.; Farley, D.; Shuman, J.; Przybyla, A.; Reilly, C.; Travis, J.
Biochemistry 26, 2289-2293, 1987
A/Title: Molecular cloning of human cathepsin G: structural similarity to mast cell and
A/Reference number: A27122; MUID:87299663; PMID:3304423
A/Accession: A27122
A/Molecule type: mRNA
A/Residues: 1-255 <S>
A/Cross-references: GB:M16117; NID:G181181; PIDN:AAA52126.1; PID:G181182
R/Maison, C.M.; Villiers, C.L.; Colomb, M.G.
J. Immunol. 147, 921-926, 1991
A/Title: Proteolysis of C3 on U937 cell plasma membranes. Purification of cathepsin G.
A/Reference number: A46471; MUID:91318179; PMID:1861080
A/Accession: A46471
A/Status: preliminary
A/Molecule type: protein
A/Residues: 21-30 <M>
A/Experimental source: monocytic cell line U937
A/Note: sequence extracted from NCBI backbone (NCBI:P:44940)
R/Bangalore, N.; Travis, J.; Onunka, V.C.; Pohl, J.; Shafer, W.M.
J. Biol. Chem. 265, 13584-13588, 1990
A/Title: Identification of the primary antimicrobial domains in human neutrophil cathepsins
A/Reference number: A37115; MUID:90337964; PMID:2116408
A/Accession: A37115
A/Status: preliminary
A/Molecule type: protein
A/Residues: 21-25; 97-103 <BAN>
R/Avril, L.E.; di Martino-Ferrer, M.; Pignede, G.; Seman, M.; Gauthier, F.
FEBS Lett. 345, 81-86, 1994
A/Title: Identification of the U-937 membrane-associated proteinase interacting with the
A/Reference number: S44427; MUID:94252410; PMID:8194606
A/Accession: S44427
A/Molecule type: protein
A/Residues: 21-52 <AVR>
A/Note: this protein was demonstrated at the surface of U-937 promonocytic cells; it can
R/Heck, L.W.; Rostand, K.S.; Hunter, F.A.; Bhowan, A.
Anal. Biochem. 158, 217-227, 1986
A/Reference number: A90031; MUID:87097924; PMID:3799965
A/Accession: A90031
A/Molecule type: protein
A/Residues: 21-38, 'E', 40, 'T', 42, 'G', 44-45 <HEC>
A/Note: residue 41 was not identified
R/Travis, J.; Giles, P.J.; Porcelli, L.; Reilly, C.F.; Baugh, R.; Powers, J.
in Protein Degradation in Health and Disease, Ciba Foundation Symposium 75, 51-68, 1980
A/Reference number: A94428
A/Accession: A94428
A/Molecule type: protein
A/Residues: 21-30, 'R', 32-38, 'E', 40, 'T' <TRA>
A/Comment: This serine proteinase is found in the azurophil granules of neutrophils and
C/Genetics:
A/Gene: GDB:CTSG
A/Cross-references: GDB:119822; OMIM:116830
A/Map position: 14q11.2-14q11.2
A/Intons: 19/1; 68/2; 113/3; 198/3
C/Superfamily: trypsin; trypsin homology
C/Keywords: glycoprotein; hydrolase; lysosome; serine proteinase
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-20/Domain: propeptide #status predicted <APT>

F;21-25/Product: cathepsin G #status experimental <MAT>
F;21-238/Domain: trypsin homology <TRY>
F;49-65,142-207,172-186/Disulfide bonds: #status predicted
F;64,108,201/Active site: His, Asp, Ser #status predicted

Query Match 29.7%; Score 338.5; DB 2; Length 255;
Best Local Similarity 36.1%; Pred. No. 9.8e-24;
Matches 82; Conservative 35; Mismatches 87; Indels 23; Gaps 7;

Qy 1 IVGRRARPHAWPFMVSLQIR---GGHFCGATLIAPNFVMSAHC-VANNVNRAVRVWL 56
Db 21 IIGRESRPSRPMAYLQIQSPAGSRGCGFLVRDFVLTAAHCWGSNIN-----VTLG 75
Qy 57 AHNLSRREPTQVFAVORIPENGT-DPVNLLNDIVILQNGSATINANVOVAQLPAQGR 115
Db 76 AHNLRRENTQOHTARRAIFHPYQNTQNDIMLLQLSRRVRNRNPNVPAQEQ 135
Qy 116 LGNGVQCLAMGWGLLGRNRIASVQLQELNTV-----VTSLCRSNVCTLVGRQA 166
Db 136 LRPGTLCTVAGWGRVSMRRG-TDTLREVQLRVQRDQCLRIFGSDPRRQICVGRDRERK 194
Qy 167 GVCFGDSGPLVNCGLTHGTASFVRGGCASGLYPDAFAPVAQFVNW 213
Db 195 AAFKGDGSGPLLCNNVAHIVSY---GKSGVPEVETRVSSFLPMI 238

RESULT 15
I55608
complement factor D (EC 3.4.21.46) precursor - rat
N/Alternate names: adipsin; C3 convertase activator; endogenous vascular elastase
C/Species: Rattus norvegicus (Norway rat)
C/Date: 19-May-2000 #sequence revision 19-May-2000 #text_change 09-Jul-2004
A/Accession: I55608; S19275
R/Zhu, L.; Wigle, D.; Hinek, A.; Kobayashi, J.; Ye, C.; Zuker, M.; Dodo, H.; Keeley, F.W.
J. Clin. Invest. 94, 1163-1171, 1994
A/Title: The endogenous vascular elastase that governs development and progression of mor-
see comments!
A/Reference number: I55608; MUID:94365184; PMID:8083356
A/Accession: I55608
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-263 <RES>
A/Cross-references: UNIPROT:P32038; GB:S73894; NID:G693721; PIDN:AAB31922.1; PID:G693722
R/Baker, B.C.; Campbell, C.J.; Grinnam, C.J.; Turcatti, G.
Biochem. J. 279, 775-779, 1991
A/Title: Purification and partial characterization of rat factor D.
A/Reference number: S19275; MUID:92061993; PMID:1953671
A/Accession: S19275
A/Molecule type: protein
A/Residues: 26-50, 'X', 52-55 <BAK>
A/Comment: Unlike its human and mouse counterparts, this molecule is N-glycosylated.
C/Complex: monomer
C/Superfamily: trypsin; trypsin homology
C/Keywords: complement alternate pathway; glycoprotein; hydrolase; plasma; serine protein
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-25/Domain: propeptide #status predicted <PRO>
F;26-263/Product: adipsin #status predicted <MAT>
F;26-249/Domain: trypsin homology <TRY>
F;46,124,256,260/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;51-67,149-215,180-196,205-230/Disulfide bonds: #status predicted
F;66,115,209/Active site: His, Asp, Ser #status predicted

Query Match 29.7%; Score 338.5; DB 1; Length 263;
Best Local Similarity 31.3%; Pred. No. 1e-23;
Matches 73; Conservative 49; Mismatches 90; Indels 21; Gaps 4;

Qy 1 IVGRRARPHAWPFMVSLQIRGGHFCGATLIAPNFVMSAHC-VANNVNRAVRVWL 59
Db 26 ILGGQEAHARPYMASVQVNGTHVCGGTLVDQWVLSAHCMDGVTQKDEWQVLLGAHS 85
Qy 60 LSRREPTQVFAVOR-IFENGTDPVLLNDIVILQNGSATINANVOVAQLPAQGR 118


```
Db      86 LSSPEPYKHLVDYQSVVHLHFGSRPDSVEDDLMLFKLSHNASLGPHVRPLPLQREDREVKP 145
Qy      119 GVOCLAMGMLGRNRGIASVLQELNVTVVVTSLCRESNVCTL-----VRGR 164
Db      146 GTLCDVAGWGVVTHAGRRPDVLQQLTVSMD----RNTCNLRTYHDGAIKNNMCAESN 200
Qy      165 QAGVCFGDSGSLVCNGLIHGIASFVRGGCASGLYPDAFAPVAQFVNWIDSII 217
Db      201 RRDTCRGDSGGPLVCGDAEAVVTWGSRVCGNRRKPGVTRVATYVPWIEENVL 253
```

Search completed: April 18, 2005, 12:50:12
Job time : 45 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 18, 2005, 12:28:28 ; Search time 178 Seconds
(without alignments)
630.030 Million cell updates/sec

Title: US-10-733-288A-4
Perfect score: 1140
Sequence: 1 IVGRRARPHAMFWLSLQ.....PDAPAPVAFVNWDSIIQR 219

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1133	99.4	267	1	ELNE_HUMAN	P08246 homo sapien
2	900	78.9	282	2	Q8MDJ1	Q8mjd1 canis famil
3	868.5	76.2	265	2	Q61515	Q61515 mus musculus
4	681	59.7	258	2	Q9GME1	Q9gme1 ornithorhyn
5	657	57.6	145	2	Q6LDP5	Q6ldp5 homo sapien
6	654	57.4	207	2	Q9Z284	Q9z284 mus musculus
7	639.5	56.1	254	2	Q8K597	Q8k597 rattus norv
8	638.5	56.0	256	1	PRN3_HUMAN	P24158 homo sapien
9	637.5	55.9	237	2	Q6LBN2	Q6lbn2 homo sapien
10	635.5	55.7	254	1	PRN3_MOUSE	Q61096 mus musculus
11	579.5	50.8	245	2	Q6DF10	Q6df10 xenopus tro
12	480	42.1	251	1	CAP7_HUMAN	P20160 homo sapien
13	428	37.5	219	1	CAP7_PIG	P80015 sus scrofa
14	390	34.2	264	2	Q8QGF6	Q8qgf6 xenopus lae
15	390	34.2	264	2	Q6GPY5	Q6gpy5 xenopus lae
16	385	33.8	258	2	Q867B0	Q867b0 canis famil
17	380	33.3	265	2	Q66KR6	Q66kr6 xenopus lae
18	379	33.2	266	1	EL1_PIG	P00772 sus scrofa
19	375	32.9	265	2	Q7SYI8	Q7syi8 xenopus lae
20	372	32.6	283	2	Q6UWY2	Q6uwy2 homo sapien
21	367	32.2	265	2	Q6GNQ0	Q6gnq0 xenopus lae
22	366.5	32.1	268	2	Q9W7Q2	Q9w7q2 paralicthyt
23	366	32.1	258	2	Q6ISM6	Q6ism6 homo sapien
24	366	32.1	266	1	EL1_RAT	P00773 rattus norv
25	365	32.0	258	1	EL1_HUMAN	Q9unil1 homo sapien
26	359	31.5	266	2	Q91X79	Q91x79 mus musculus
27	357.5	31.4	249	2	Q9W7Q1	Q9w7q1 paralicthyt
28	357	31.3	266	2	Q9D936	Q9d936 mus musculus
29	356	31.2	266	1	EL1_BOVIN	Q28153 bos taurus
30	355	31.1	278	2	Q68FN6	Q68fn6 brachydanio
31	354	31.1	266	2	Q46644	Q46644 macaca fasc

RESULT 1									
ID ELNE_HUMAN STANDARD; PRT; 267 AA.									
AC	P08246	P09649;							Q6dgm4 brachydanio
DT	01-AUG-1988	(Rel. 08, Created)							P80931 ovis aries
DT	01-AUG-1988	(Rel. 08, Last sequence update)							Q6azc0 brachydanio
DT	25-OCT-2004	(Rel. 45, Last annotation update)							Q7sig3 salmo salar
DE	Leukocyte elastase precursor (EC 3.4.21.37) (Neutrophil elastase) (PMN)								
DE	elastase) (Bone marrow serine protease) (Medullasin).								
GN	Name=ELA2;								
OS	Homo sapiens (Human).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.								
OX	NCBI_TaxID=9606;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE=89374820; PubMed=2775493;								
RA	Farley D., Travis J., Salvesen G.;								
RT	"The human neutrophil elastase gene. Analysis of the nucleotide								
RT	sequence reveals three distinct classes of repetitive DNA.";								
RL	Biol. Chem. Hoppe-Seyler 370:737-744(1989).								
RN	[2]								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE=89067782; PubMed=3479752;								
RA	Nakamura H., Okano K., Aoki Y., Shimizu H., Naruto M.;								
RT	"Nucleotide sequence of human bone marrow serine protease (medullasin)								
RT	gene.";								
RL	Nucleic Acids Res. 15:9601-9601(1987).								
RN	[3]								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE=89008342; PubMed=2902087;								
RA	Takahashi H., Nukiwa T., Yoshimura K., Quick C.D., States D.J.,								
RA	Holmes M.D., Whang-Peng J., Knutsen T., Crystal R.G.;								
RT	"Structure of the human neutrophil elastase gene.";								
RL	J. Biol. Chem. 263:14739-14747(1988).								
RN	[4]								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE=90211319; PubMed=2322278;								
RA	Okano K., Aoki Y., Shimizu H., Naruto M.;								
RT	"Functional expression of human leukocyte elastase (HLE)/medullasin in								
RT	eukaryotic cells.";								
RL	Biochem. Biophys. Res. Commun. 167:1326-1332(1990).								
RN	[5]								
RP	SEQUENCE FROM N.A., AND VARIANTS ILE-219; LEU-257 AND LEU-262.								
RA	Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N.,								
RA	Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S.,								
RA	Sherwood J.K., Sherwood A.M., Leithauser B.J., Nickerson D.A.;								
RT	"NIHES-SNPs, environmental genome project, NIHES ES15478, Department								
RT	of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";								
RL	Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.								
RN	[6]								
RP	SEQUENCE OF 30-267 FROM N.A.								
RX	MEDLINE=89032918; PubMed=2822677;								
RA	Okano K., Aoki Y., Sakurai T., Kajitani M., Kanai S., Shimazu T.,								

Q6dgm4 brachydanio
P80931 ovis aries
Q6azc0 brachydanio
Q7sig3 salmo salar
Q86822 homo sapien
Q9gln2 bos taurus
P28293 mus musculus
P12544 homo sapien
Q6azf9 xenopus lae
Q8n4e0 homo sapien
Q86vj5 homo sapien
P00746 homo sapien
Q8wzb4 homo sapien
P49864 rattus norv

ALIGNMENTS

RA	Shimizu H., Naruto M.;	CC	dominant disease in which blood-cell production from the bone
RT	"Molecular cloning of complementary DNA for human medullasin: an	CC	marrow oscillates with 21-day periodicity. Circulating neutrophils
RT	inflammatory serine protease in bone marrow cells.";	CC	vary between almost normal numbers and zero. During intervals of
RL	J. Biochem. 102:13-16(1987).	CC	neutropenia, affected individuals are at risk for opportunistic
RN	[7]	CC	infection. Monocytes, platelets, lymphocytes and reticulocytes
RP	SEQUENCE OF 75-267 FROM N.A.	CC	also cycle with the same frequency.
RX	MEDLINE=88115408; PubMed=3422232;	CC	-!- SIMILARITY: Belongs to the peptidase S1 family. Elastase
RA	Takahashi H., Nukiwa T., Bassett P., Cystal R.G.;	CC	subfamily.
RT	"Myelomonocytic cell lineage expression of the neutrophil elastase	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
RL	gene.";	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
RN	J. Biol. Chem. 263:2543-2547(1988).	CC	the European Bioinformatics Institute. There are no restrictions on its
RP	SEQUENCE OF 30-247.	CC	use by non-profit institutions as long as its content is in no way
RX	MEDLINE=87175647; PubMed=3550808;	CC	modified and this statement is not removed. Usage by and for commercial
RA	Sinha S., Watorek W., Karr S., Giles J., Bode W., Travis J.;	CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
RT	"Primary structure of human neutrophil elastase.";	CC	or send an email to license@isb-sib.ch).
RN	Proc. Natl. Acad. Sci. U.S.A. 84:2228-2232(1987).	CC	-----
RP	SEQUENCE OF 262-267.	DR	EMBL; J03545; AAA52378.1; -.
RX	MEDLINE=91315473; PubMed=1859409;	DR	EMBL; Y00477; CRA68537.1; -.
RA	Aoki Y., Hase T.;	DR	EMBL; X05875; CRA29299.1; -.
RT	"The primary structure and elastolytic activity of medullasin (a	DR	EMBL; X05875; CRA29300.1; ALT_INIT.
RL	serine protease of bone marrow).";	DR	EMBL; M20203; AAA36359.1; -.
RN	Biochem. Biophys. Res. Commun. 178:501-506(1991).	DR	EMBL; M20199; AAA36359.1; JOINED.
RP	PRELIMINARY SEQUENCE OF 30-103.	DR	EMBL; M20200; AAA36359.1; JOINED.
RA	Travis J., Giles P.J., Porcelli L., Reilly C.F., Baugh R., Powers J.;	DR	EMBL; AY596461; AAA89303.1; -.
RT	"In protein degradation in health and disease, Ciba Foundation	DR	EMBL; M34379; AAA36173.1; -.
RL	Symposium, pp.75:51-68, Excerpta Medica, Amsterdam and Oxford (1980).	DR	EMBL; D00187; BAA00128.1; -.
RN	[11]	DR	PIR; A31976; ELHUL.
RP	SEQUENCE OF 30-49.	DR	PDB; 1B0F; X-ray; A=30-247.
RX	MEDLINE=89315847; PubMed=2501794;	DR	PDB; 1H1B; X-ray; A/B=30-247.
RA	Gabay J.E., Scott R.W., Campanelli D., Griffith J., Wilde C.,	DR	PDB; 1HNE; X-ray; E=30-247.
RT	Marra M.N., Seeger M., Nathan C.F.;	DR	PDB; 1PPF; X-ray; E=30-247.
RL	"Antibiotic proteins of human polymorphonuclear leukocytes.";	DR	PDB; 1PPG; X-ray; E=30-247.
RN	Proc. Natl. Acad. Sci. U.S.A. 86:5610-5614(1989).	DR	MEROPS; S01.131; -.
RP	X-RAY CRYSTALLOGRAPHY (1.84 ANGSTROMS).	DR	Genew; HGNC:3309; ELA2.
RA	Navia M.A., McKeever B.M., Springer J.P., Lin T.-Y., Williams H.R.,	DR	MIM; 130130; -.
RT	Fluder E.M., Dorn C.P., Hoogsteen K.;	DR	GO; GO:0004234; F:macrophage elastase activity; TAS.
RL	"Structure of human neutrophil elastase in complex with a peptide	DR	InterPro; IPR009003; Pept_Ser_Cys.
RN	chloromethyl ketone inhibitor at 1.84-A resolution.";	DR	InterPro; IPR001254; Peptidase_S1.
RP	Proc. Natl. Acad. Sci. U.S.A. 86:7-11(1989).	DR	InterPro; IPR001314; Peptidase_S1A.
RX	X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).	DR	Pfam; PF00889; Trypsin; 1
RA	MEDLINE=88271660; PubMed=3391280; DOI=10.1016/0014-5793(88)80118-2;	DR	PRINTS; PR00722; CHYMOTRYPSIN.
RT	"The refined 2.3-A crystal structure of human leukocyte elastase in a	DR	PROSITE; PS00240; TRYPSIN_DOM; 1.
RL	complex with a valine chloromethyl ketone inhibitor.";	DR	PROSITE; PS00134; TRYPSIN_HIS; 1.
RN	FEBS Lett. 234:367-373(1988).	KW	3D-structure; Direct protein sequencing; Disease mutation;
RP	X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).	KW	Glycoprotein; Hydrolase; Polymorphism; Serine protease; Signal.
RA	Bode W., Wei A.-Z., Huber R., Meyer E., Travis J., Neumann S.;	FT	SIGNAL 1 27 Potential.
RT	"X-ray crystal structure of the complex of human leukocyte elastase	FT	PROPEP 28 29
RL	(PMN elastase) and the third domain of the turkey ovomucoid	FT	CHAIN 30 267
RN	inhibitor.";	FT	ACT_SITE 70 70
RX	MEDLINE=20047772; PubMed=3640709;	FT	ACT_SITE 117 117
RA	Bode W., Wei A.-Z., Huber R., Meyer E., Travis J., Neumann S.;	FT	ACT_SITE 202 202
RT	"X-ray crystal structure of the complex of human leukocyte elastase	FT	DISULFID 55 71
RL	(PMN elastase) and the third domain of the turkey ovomucoid	FT	DISULFID 151 208
RN	inhibitor.";	FT	DISULFID 181 187
RX	MEDLINE=88271660; PubMed=3391280; DOI=10.1016/0014-5793(88)80118-2;	FT	DISULFID 198 223
RA	Wei A.-Z., Mayr I., Bode W.;	FT	CARBOHYD 88 88
RT	"The refined 2.3-A crystal structure of human leukocyte elastase in a	FT	CARBOHYD 124 124
RL	complex with a valine chloromethyl ketone inhibitor.";	FT	CARBOHYD 173 173
RN	FEBS Lett. 234:367-373(1988).	FT	VARIANT 32 32
RP	X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).	FT	VARIANT 177 177
RA	Bode W., Wei A.-Z., Huber R., Meyer E., Travis J., Neumann S.;	FT	VARIANT 191 191
RT	"X-ray crystal structure of the complex of human leukocyte elastase	FT	VARIANT 219 219
RL	(PMN elastase) and the third domain of the turkey ovomucoid	FT	VARIANT 257 257
RN	inhibitor.";	FT	VARIANT 262 262
RX	MEDLINE=20047772; PubMed=3640709;	FT	
RA	Bode W., Wei A.-Z., Huber R., Meyer E., Travis J., Neumann S.;	FT	
RT	"X-ray crystal structure of the complex of human leukocyte elastase	FT	
RL	(PMN elastase) and the third domain of the turkey ovomucoid	FT	
RN	inhibitor.";	FT	
RX	MEDLINE=88271660; PubMed=3391280; DOI=10.1016/0014-5793(88)80118-2;	FT	
RA	Wei A.-Z., Mayr I., Bode W.;	FT	
RT	"The refined 2.3-A crystal structure of human leukocyte elastase in a	FT	
RL	complex with a valine chloromethyl ketone inhibitor.";	FT	
RN	FEBS Lett. 234:367-373(1988).	FT	
RP	X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).	FT	
RA	Bode W., Wei A.-Z., Huber R., Meyer E., Travis J., Neumann S.;	FT	
RT	"X-ray crystal structure of the complex of human leukocyte elastase	FT	
RL	(PMN elastase) and the third domain of the turkey ovomucoid	FT	
RN	inhibitor.";	FT	
RX	MEDLINE=20047772; PubMed=3640709;	FT	
RA	Bode W., Wei A.-Z., Huber R., Meyer E., Travis J., Neumann S.;	FT	
RT	"X-ray crystal structure of the complex of human leukocyte elastase	FT	
RL	(PMN elastase) and the third domain of the turkey ovomucoid	FT	
RN	inhibitor.";	FT	
RX	MEDLINE=88271660; PubMed=3391280; DOI=10.1016/0014-5793(88)80118-2;	FT	
RA	Wei A.-Z., Mayr I., Bode W.;	FT	
RT	"The refined 2.3-A crystal structure of human leukocyte elastase in a	FT	
RL	complex with a valine chloromethyl ketone inhibitor.";	FT	
RN	FEBS Lett. 234:367-373(1988).	FT	
RP	X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).	FT	
RA	Bode W., Wei A.-Z., Huber R., Meyer E., Travis J., Neumann S.;	FT	
RT	"X-ray crystal structure of the complex of human leukocyte elastase	FT	
RL	(PMN elastase) and the third domain of the turkey ovomucoid	FT	
RN	inhibitor.";	FT	
RX	MEDLINE=20047772; PubMed=3640709;	FT	
RA	Bode W., Wei A.-Z., Huber R., Meyer E., Travis J., Neumann S.;	FT	
RT	"X-ray crystal structure of the complex of human leukocyte elastase	FT	
RL	(PMN elastase) and the third domain of the turkey ovomucoid	FT	
RN	inhibitor.";	FT	
RX	MEDLINE=88271660; PubMed=3391280; DOI=10.1016/0014-5793(88)80118-2;	FT	
RA	Wei A.-Z., Mayr I., Bode W.;	FT	
RT	"The refined 2.3-A crystal structure of human leukocyte elastase in a	FT	
RL	complex with a valine chloromethyl ketone inhibitor.";	FT	
RN	FEBS Lett. 234:367-373(1988).	FT	
RP	X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).	FT	
RA	Bode W., Wei A.-Z., Huber R., Meyer E., Travis J., Neumann S.;	FT	
RT	"X-ray crystal structure of the complex of human leukocyte elastase	FT	
RL	(PMN elastase) and the third domain of the turkey ovomucoid	FT	
RN	inhibitor.";	FT	
RX	MEDLINE=20047772; PubMed=3640709;	FT	
RA	Bode W., Wei A.-Z., Huber R., Meyer E., Travis J., Neumann S.;	FT	
RT	"X-ray crystal structure of the complex of human leukocyte elastase	FT	
RL	(PMN elastase) and the third domain of the turkey ovomucoid	FT	
RN	inhibitor.";	FT	
RX	MEDLINE=88271660; PubMed=3391280; DOI=10.1016/0014-5793(88)80118-2;	FT	
RA	Wei A.-Z., Mayr I., Bode W.;	FT	
RT	"The refined 2.3-A crystal structure of human leukocyte elastase in a	FT	
RL	complex with a valine chloromethyl ketone inhibitor.";	FT	
RN	FEBS Lett. 234:367-373(1988).	FT	
RP	X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).	FT	
RA	Bode W., Wei A.-Z., Huber R., Meyer E., Travis J., Neumann S.;	FT	
RT	"X-ray crystal structure of the complex of human leukocyte elastase	FT	
RL	(PMN elastase) and the third domain of the turkey ovomucoid	FT	
RN	inhibitor.";	FT	
RX	MEDLINE=20047772; PubMed=3640709;	FT	
RA	Bode W., Wei A.-Z., Huber R., Meyer E., Travis J., Neumann S.;	FT	
RT	"X-ray crystal structure of the complex of human leukocyte elastase	FT	
RL	(PMN elastase) and the third domain of the turkey ovomucoid	FT	
RN	inhibitor.";	FT	
RX	MEDLINE=88271660; PubMed=3391280; DOI=10.1016/0014-5793(88)80118-2;	FT	
RA	Wei A.-Z., Mayr I., Bode W.;	FT	
RT	"The refined 2.3-A crystal structure of human leukocyte elastase in a	FT	
RL	complex with a valine chloromethyl ketone inhibitor.";	FT	
RN	FEBS Lett. 234:367-373(1988).	FT	
RP	X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).	FT	
RA	Bode W., Wei A.-Z., Huber R., Meyer E., Travis J., Neumann S.;	FT	
RT	"X-ray crystal structure of the complex of human leukocyte elastase	FT	
RL	(PMN elastase) and the third domain of the turkey ovomucoid	FT	
RN	inhibitor.";	FT	
RX	MEDLINE=20047772; PubMed=3640709;	FT	
RA	Bode W., Wei A.-Z., Huber R., Meyer E., Travis J., Neumann S.;	FT	
RT	"X-ray crystal structure of the complex of human leukocyte elastase	FT	
RL	(PMN elastase) and the third domain of the turkey ovomucoid	FT	
RN	inhibitor.";	FT	
RX	MEDLINE=88271660; PubMed=3391280; DOI=10.1016/0014-5793(88)80118-2;	FT	
RA	Wei A.-Z., Mayr I., Bode W.;	FT	
RT	"The refined 2.3-A crystal structure of human leukocyte elastase in a	FT	
RL	complex with a valine chloromethyl ketone inhibitor.";	FT	
RN	FEBS Lett. 234:367-373(1988).	FT	
RP	X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).	FT	
RA	Bode W., Wei A.-Z., Huber R., Meyer E., Travis J., Neumann S.;	FT	
RT	"X-ray crystal structure of the complex of human leukocyte elastase	FT	
RL	(PMN elastase) and the third domain of the turkey ovomucoid	FT	
RN	inhibitor.";	FT	
RX	MEDLINE=20047772; PubMed=3640709;	FT	
RA	Bode W., Wei A.-Z., Huber R., Meyer E., Travis J., Neumann S.;	FT	
RT	"X-ray crystal structure of the complex of human leukocyte elastase	FT	
RL	(PMN elastase) and the third domain of the turkey ovomucoid	FT	
RN	inhibitor.";	FT	
RX	MEDLINE=88271660; PubMed=3391280; DOI=10.1016/0014-5793(88)80118-2;	FT	
RA	Wei A.-Z., Mayr I., Bode W.;	FT	
RT	"The refined 2.3-A crystal structure of human leukocyte elastase in a	FT	
RL	complex with a valine chloromethyl ketone inhibitor.";	FT	
RN	FEBS Lett. 234:367-373(1988).	FT	
RP	X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).	FT	
RA	Bode W., Wei A.-Z., Huber R., Meyer E., Travis J., Neumann S.;	FT	
RT	"X-ray crystal structure of the complex of human leukocyte elastase	FT	
RL	(PMN elastase) and the third domain of the turkey ovomucoid	FT	
RN	inhibitor.";	FT	
RX	MEDLINE=20047772; PubMed=3640709;	FT	
RA	Bode W., Wei A.-Z., Huber R., Meyer E., Travis J., Neumann S.;	FT	
RT	"X-ray crystal structure of the complex of human leukocyte elastase	FT	
RL	(PMN elastase) and the third domain of the turkey ovomucoid	FT	
RN	inhibitor.";	FT	
RX	MEDLINE=88271660; PubMed=3391280; DOI=10.1016/0014-5793(88)80118-2;	FT	
RA	Wei A.-Z., Mayr I., Bode W.;	FT	
RT	"The refined 2.3-A crystal structure of human leukocyte elastase in a	FT	
RL	complex with a valine chloromethyl ketone inhibitor.";	FT	
RN	FEBS Lett. 234:367-373(1988).	FT	
RP	X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).	FT	
RA	Bode W., Wei A.-Z., Huber R., Meyer E., Travis J., Neumann S.;	FT	
RT	"X-ray crystal structure of the complex of human leukocyte elastase	FT	
RL	(PMN elastase) and the third domain of the turkey ovomucoid	FT	
RN	inhibitor.";	FT	
RX	MEDLINE=20047772; PubMed=3640709;	FT	
RA	Bode W., Wei A.-Z., Huber R., Meyer E., Travis J., Neumann S.;	FT	
RT	"X-ray crystal structure of the complex of human leukocyte elastase	FT	
RL	(PMN elastase) and the third domain of the turkey ovomucoid	FT	
RN	inhibitor.";	FT	
RX	MEDLINE=88271660; PubMed=3391280; DOI=10.1016/0014-5793(88)80118-2;	FT	
RA	Wei A.-Z., Mayr I., Bode W.;	FT	
RT	"The refined 2.3-A crystal structure of human leukocyte elastase in a	FT	
RL	complex with a valine chloromethyl ketone inhibitor.";	FT	
RN	FEBS Lett. 234:367-373(1988).	FT	
RP	X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).	FT	
RA	Bode W., Wei A.-Z., Huber R., Meyer E., Travis J., Neumann S.;	FT	
RT	"X-ray crystal structure of the complex of human leukocyte elastase	FT	
RL	(PMN elastase) and the third domain of the turkey ovomucoid	FT	
RN	inhibitor.";	FT	
RX	MEDLINE=20047772; PubMed=3640709;	FT	
RA	Bode W., Wei A.-Z., Huber R., Meyer E., Travis J., Neumann S.;	FT	
RT	"X-ray crystal structure of the complex of human leukocyte elastase	FT	
RL	(PMN elastase) and the third domain of the turkey ovomucoid	FT	
RN	inhibitor.";	FT	
RX	MEDLINE=88271660; PubMed=3391280; DOI=10.1016/0014-5793(88)80118-2;	FT	
RA	Wei A.-Z., Mayr I., Bode W.;	FT	
RT	"The refined 2.3-A crystal structure of human leukocyte elastase in a	FT	
RL	complex with a valine chloromethyl ketone inhibitor.";	FT	
RN	FEBS Lett. 234:367-373(1988).	FT	
RP	X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).	FT	
RA	Bode W., Wei A.-Z., Huber R., Meyer E., Travis J., Neumann S.;	FT	
RT	"X-ray crystal structure of the complex of human leukocyte elastase	FT	
RL	(PMN elastase) and the third domain of the turkey ovomucoid	FT	
RN	inhibitor.";	FT	
RX	MEDLINE=20047772; PubMed=3640709;	FT	
RA	Bode W., Wei A.-Z., Huber R., Meyer E., Travis J., Neumann S.;	FT	
RT	"X-ray crystal structure of the complex of human leukocyte elastase	FT	
RL	(PMN elastase) and the third domain of the turkey ovomucoid	FT	
RN	inhibitor.";	FT	
RX	MEDLINE=88271660; PubMed=3391280; DOI=10.1016/0014-5793(88)80118-2;	FT	
RA	Wei A.-Z., Mayr I., Bode W.;	FT	
RT	"The refined 2.3-A crystal structure of human leukocyte elastase in a	FT	
RL	complex with a valine chloromethyl ketone inhibitor.";	FT	
RN	FEBS Lett. 234:367-373(1988).	FT	
RP	X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).	FT	
RA	Bode W., Wei A.-Z., Huber R., Meyer E., Travis J., Neumann S.;	FT	
RT	"X-ray crystal structure of the complex of human leukocyte elastase	FT	
RL	(PMN elastase) and the third domain of the turkey ovomucoid	FT	
RN	inhibitor.";	FT	
RX	MEDLINE=20047772; PubMed=3640709;	FT	
RA	Bode W., Wei A.-Z., Huber R., Meyer E., Travis J., Neumann S.;	FT	
RT	"X-ray crystal structure of the complex of human leukocyte elastase	FT	
RL	(PMN elastase) and the third domain of the turkey ovomucoid	FT	
RN	inhibitor.";	FT	
RX	MEDLINE=88271660; PubMed=3391280; DOI=10.1016/0014-5793(88)80118-2;	FT	
RA	Wei A.-Z., Mayr I., Bode W.;	FT	
RT	"The refined 2.3-A crystal structure of human leukocyte elastase in a	FT	
RL	complex with a valine chloromethyl ketone inhibitor.";	FT	
RN	FEBS Lett. 234:367-373(1988).	FT	
RP	X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).	FT	
RA	Bode W., Wei A.-Z., Huber R., Meyer E., Travis J., Neumann S.;	FT	
RT	"X-ray crystal structure of the complex of human leukocyte elastase	FT	
RL	(PMN elastase) and the third domain of the turkey ovomucoid	FT	
RN	inhibitor.";	FT	
RX	MEDLINE=20047772; PubMed=3640709;	FT	
RA	Bode W., Wei A.-Z., Huber R., Meyer E., Travis J., Neumann S.;	FT	
RT	"X-ray crystal structure of the complex of human leukocyte elastase	FT	
RL	(PMN elastase) and the third domain of the turkey ovomucoid	FT	
RN	inhibitor.";	FT	
RX	MEDLINE=88271660; PubMed=3391280; DOI=10.1016/0014-5793(88)80118-2;	FT	
RA	Wei A.-Z., Mayr I., Bode W.;	FT	
RT	"The refined 2.3-A crystal structure of human leukocyte elastase in a	FT	
RL	complex with a valine chloromethyl ketone inhibitor.";	FT	
RN	FEBS Lett. 234:367-373(1988).	FT	
RP	X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).	FT	
RA	Bode W., Wei A.-Z., Huber R., Meyer E., Travis J., Neumann S.;	FT	
RT	"X-ray crystal structure of the complex of human leukocyte elastase	FT	
RL	(PMN elastase) and the third domain of the turkey ovomucoid	FT	
RN	inhibitor.";	FT	
RX	MEDLINE=20047772; PubMed=3640709;	FT	
RA	Bode W., Wei A.-Z., Huber R., Meyer E., Travis J., Neumann S.;	FT	
RT	"X-ray crystal structure of the complex of human leukocyte elastase	FT	
RL	(PMN elastase) and the third domain of the turkey ovomucoid	FT	
RN	inhibitor.";	FT	
RX	MEDLINE=88271660; PubMed=3391280; DOI=10.1016/0014-5793(88)80118-2;	FT	
RA	Wei A.-Z., Mayr I., Bode W.;	FT	

```

FT FT CONFLICT 107 107 /FTId=VAR 019239.
FT FT CONFLICT 107 107 N -> D (in Ref. 7).

Query Match 99.4%; Score 1133; DB 1; Length 267;
Best Local Similarity 99.5%; Pred. No. 2.1e-94;
Matches 218; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 IVGGRARPHAWPFMVSLQLRGHCATLIAPNFVMSAAHCVANVRAVRVVLGAHNL 60
Db IVGGRARPHAWPFMVSLQLRGHCATLIAPNFVMSAAHCVANVRAVRVVLGAHNL 90
QY 61 SRREPTQVFAVQIFENGCTDPVNLNDIVILQNGSATINANVOVAQLPAQGRRLNGV 120
Db 90 SRREPTQVFAVQIFENGCTDPVNLNDIVILQNGSATINANVOVAQLPAQGRRLNGV 149
QY 121 QCLAMGWLLGRNRGIASVLQELNVTVTSLCRSSNVCTLVGRQAGVCFGDSGPLVCN 180
Db 150 QCLAMGWLLGRNRGIASVLQELNVTVTSLCRSSNVCTLVGRQAGVCFGDSGPLVCN 209
QY 181 GLIHGIASFVGGCAGLYPDAPAPVAQFVNWIDSIIOR 219
Db 210 GLIHGIASFVGGCAGLYPDAPAPVAQFVNWIDSIIOR 248

RESULT 2
Q8MJD1 PRELIMINARY; PRT; 282 AA.
ID Q8MJD1
AC Q8MJD1
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Neutrophil elastase.
GN Name=ELA2;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Katen L.J., Aprikyan A.G., Dale D.C., Osborne W.R.A.;
RT "Molecular Cloning and Sequencing of the Canine Neutrophil Elastase
  CDNA."
RL DNA Seq. 13:221-223 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Benson K.F., Albani D., Person R.E., Horwitz M.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AF494190; AAM95916.1; -
DR EMBL; AY221639; AAO65978.1; -
DR PIR; A60551; A60551.
DR HSSP; P08246; 1PPF.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 282 AA; 29920 MW; B6F31953BFA4F9B3 CRC64;

Query Match 78.9%; Score 900; DB 2; Length 282;
Best Local Similarity 77.6%; Pred. No. 2.8e-73;
Matches 170; Conservative 21; Mismatches 28; Indels 0; Gaps 0;

QY 1 IVGGRARPHAWPFMVSLQLRGHCATLIAPNFVMSAAHCVANVRAVRVVLGAHNL 60
Db IVGGRARPHAWPFMVSLQLRGHCATLIAPNFVMSAAHCVANVRAVRVVLGAHNL 90
QY 61 SRREPTQVFAVQIFENGCTDPVNLNDIVILQNGSATINANVOVAQLPAQGRRLNGV 120
Db 90 SRREPTQVFAVQIFENGCTDPVNLNDIVILQNGSATINANVOVAQLPAQGRRLNGV 149
QY 121 QCLAMGWLLGRNRGIASVLQELNVTVTSLCRSSNVCTLVGRQAGVCFGDSGPLVCN 180
Db 150 QCLAMGWLLGRNRGIASVLQELNVTVTSLCRSSNVCTLVGRQAGVCFGDSGPLVCN 209
QY 181 GLIHGIASFVGGCAGLYPDAPAPVAQFVNWIDSIIOR 219
Db 210 GLIHGIASFVGGCAGLYPDAPAPVAQFVNWIDSIIOR 248

RESULT 3
Q61515 PRELIMINARY; PRT; 265 AA.
ID Q61515
AC Q61515;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Neutrophil elastase.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Nuchprayoon I., Meyers S., Scott L.M., Suzov J., Hiebert S.;
RT "PEBP2/CBP, the murine homolog of the human myeloid AML1 and PEBP2
  beta/CBP beta proto-oncoproteins, regulates the murine myeloperoxidase
  and neutrophil elastase genes in immature myeloid cells."
RL Mol. Cell. Biol. 14:5558-5568 (1994).
CC -1- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; U04962; AAB60670.1; -
DR EMBL; U06076; AAB60670.1; JOINED.
DR PIR; I48679; I48679.
DR HSSP; P08246; 1PPF.
DR MEROPS; S01.131; -.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 265 AA; 28654 MW; 8744D5CE3A72E09D CRC64;

Query Match 76.2%; Score 868.5; DB 2; Length 265;
Best Local Similarity 75.9%; Pred. No. 1.9e-70;
Matches 167; Conservative 19; Mismatches 33; Indels 1; Gaps 1;

QY 1 IVGGRARPHAWPFMVSLQLRGHCATLIAPNFVMSAAHCVANVRAVRVVLGAHNL 60
Db IVGGRARPHAWPFMVSLQLRGHCATLIAPNFVMSAAHCVANVRAVRVVLGAHNL 88
QY 61 SRREPTQVFAVQIFENGCTDPVNLNDIVILQNGSATINANVOVAQLPAQGRRLNGV 120
Db 89 RQERTRQIFVQIGFENGCTDPVNLNDIVILQNGSATINANVOVAQLPAQGRRLNGV 148
QY 121 QCLAMGWLLGRNRGIASVLQELNVTVTSLC-RRSNVCTLVGRQAGVCFGDSGPLVCN 179

```

Db 149 PCLANGWGLTNRSPSPVQLNLTAVVTVNMCPREVVNCTLVPRRQAGICFGDGGPLVC 208
QY 180 NGLIHGIAFVRGGCAGSLGYPDAFAPVAQFVNWIDSIOR 219
Db 209 NNVLQGDIDSFIRGGCGSLGYPDAFAPVGFVDWINSIIR 248

RESULT 4
Q9GME1 PRELIMINARY; PRT; 258 AA.
AC Q9GME1; MEDLINE=21015017; PubMed=11132153; DOI=10.1007/s002510000246;
DT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE N-elastase.
OS Ornithorhynchus anatinus (Duckbill platypus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus.
OX NCBI_TaxID=9258;
FN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21015017; PubMed=11132153; DOI=10.1007/s002510000246;
RA Poorafshar M., Aveskogh M., Munday B., Hellman L.;
RT "Identification and structural analysis of four serine proteases in a
monotreme, the platypus, Ornithorhynchus anatinus."
RL Immunogenetics 52:19-28 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Poorafshar M.M.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AF275652; AAG00451.1; -.
DR HSSP; P20160; 1A7S.
DR MEROPS; S01.131; -.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0008233; F:trypsin activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase S1A.
DR InterPro; IPR009003; Pept Ser Cys.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRY SP; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydroxylase; Protease; Serine protease.
SQ SEQUENCE 258 AA; 28165 MW; 2E1752C300A36138 CRC64;

Query Match 59.7%; Score 681; DB 2; Length 258;
Best Local Similarity 58.7%; Pred. No. 1.7e-53;
Matches 131; Conservative 38; Mismatches 44; Indels 10; Gaps 4;
QY 1 IVGGRRARPHAFVMSVLSL-RGGHFCGATLIAPFVMSAAHCVANVAVRVVLGAHN 59
Db 24 IVGAVMLFPLA-PYIASLQRNRGGHFCGGLTHQQFVMTAAHCINSRVSRVVLGAHN 82
QY 60 LSRRETRQVAVORIFENGTPDVLNLDIVILQNGSATINANVQVQLPAQRRRLQNG 119
Db 83 LRAQESTRTQYSVDQIFENGFSPTQLNDILLVLSRPVTLNANVQLARLPQONQVSG 142
QY 120 VQCLANGWGLLGRNRGI---ASVQLQELNVTVTSLCRSNVCTLVGRQAGVCFDGGSP 176
Db 143 TQCLANGWG-----KAIMPAAHILQELNVTVTNQCQRIICTLVPSRRAGICFGDGGP 197
QY 177 LVNGLIHGIAFVRGGCAGSLGYPDAFAPVAQFVNWIDSIOR 219
Db 198 LVNCNGIVHGDIDSFVRGGCAGSLGYPDAFAPVGFVDWINSIIR 240

RESULT 5
Q6LDP5

Q6LDP5 PRELIMINARY; PRT; 145 AA.
AC Q6LDP5; MEDLINE=89076526; PubMed=2462434;
DT 03-JUL-2004 (T-EMBLrel. 27, Created)
DT 03-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Neutrophil elastase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
FN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89076526; PubMed=2462434;
RA Farley D., Salvessen G.S., Travis J.;
RT "Molecular cloning of human neutrophil elastase."
RL Biol. Chem. Hoppe-Seyler 369:3-7 (1988).
DR EMBL; M27783; AAA35792.1; -.
DR HSSP; P08246; 1B0F.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR009003; Pept Ser Cys.
DR Pfam; PF00089; Trypsin_1;
DR SMART; SM00020; TRY SP; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KW Hydroxylase; Protease; Serine protease.
FT NON TER 1
FT CHAIN <1 125 Potential.
SQ SEQUENCE 145 AA; 15278 MW; 9ABE1141003AB00D CRC64;
Query Match 57.6%; Score 657; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 1.4e-51;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 94 LNSGATINANVQVQLPAQRRLLGNGVQCLANGGLGRNRGIAASVQLQELNVTVTSLCR 153
Db 1 LNSGATINANVQVQLPAQRRLLGNGVQCLANGGLGRNRGIAASVQLQELNVTVTSLCR 60
QY 154 RSNVCTLVGRQAGVCFDGGSPPLVNCGLIHGIAFVRGGCAGSLGYPDAFAPVAQFVNW 213
Db 61 RSNVCTLVGRQAGVCFDGGSPPLVNCGLIHGIAFVRGGCAGSLGYPDAFAPVAQFVNW 120
QY 214 DSIQIR 219
Db 121 DSIQIR 126
RESULT 6
Q9Z284 PRELIMINARY; PRT; 207 AA.
AC Q9Z284; MEDLINE=129/SVJ;
DT 01-MAY-1999 (T-EMBLrel. 10, Created)
DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Neutrophil elastase.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
FN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RA Sturrock A., Franklin K.F., Wu S.Q., Hoidal J.R.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AF082186; AAC79702.1; -.
DR HSSP; P08246; 1PPF.
DR MEROPS; S01.131; -.
DR MGD; MGI:95316; Ela2.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.

```

DR GO: 0008233; F:peptidase activity; IEA.
DR GO: 0004295; F:trypsin activity; IEA.
DR GO: 0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR001254; Peptidase_S1.
DR InterPro: IPR001314; Peptidase_S1A.
DR InterPro: IPR009003; Pept_Ser_Cys.
DR Pfam: PF00089; Trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM0020; Tryp_SPC; 1.
DR PROSITE: PS0240; TRYPSIN_DOM; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 207 AA; 22526 MW; 1F4B834DD173DEE CRC64;

Query Match
Best Local Similarity 57.4%; Score 654; DB 2; Length 207;
Matches 131; Conservative 12; Mismatches 26; Indels 2; Gaps 2;

QY 1 IVGGRARPHAWPMVSLQRLGCGATLIAPNFVMSAAHCVANVNVRAVRVVLGNHL 60
DB 1 IVGGRARPHAWPMVSLQRLGCGATLIAPNFVMSAAHCVANVNVRAVRVVLGNHL 60
QY 29 IVGGRARPHAWPMVSLQRLGCGATLIAPNFVMSAAHCVANVNVRAVRVVLGNHL 87
DB 29 IVGGRARPHAWPMVSLQRLGCGATLIAPNFVMSAAHCVANVNVRAVRVVLGNHL 87
QY 61 SRREPTRQVAVORIFENGDPVNLNDIVILQNGSATINANVQVAPLPAQGRRLNGV 120
DB 61 SRREPTRQVAVORIFENGDPVNLNDIVILQNGSATINANVQVAPLPAQGRRLNGV 120
QY 88 RQERTQTFVSORIFENGDPQLNDIVILQNGSATINANVQVAPLPAQGRRLNGV 147
DB 88 RQERTQTFVSORIFENGDPQLNDIVILQNGSATINANVQVAPLPAQGRRLNGV 147
QY 121 QCLAMGGLGRNGRIASVLOELNVVTSLSLRRSNVCTLVGRGAGVCF 170
DB 121 QCLAMGGLGRNGRIASVLOELNVVTSLSLRRSNVCTLVGRGAGVCF 170
QY 148 PCLAMGGLGRNGRIASVLOELNVVTSLSLRRSNVCTLVGRGAGVCF 198
DB 148 PCLAMGGLGRNGRIASVLOELNVVTSLSLRRSNVCTLVGRGAGVCF 198

RESULT 7
Q8K597 PRELIMINARY; PRT; 254 AA.
ID AC Q8K597;
DC Q8K597;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Proteinase 3 (EC 3.4.21.76).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SQ SEQUENCE FROM N.A.
RA Rao N.V., Rao G.N., Hoidal J.R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AF503440; AAM27444.1; -.
DR HSSP; P18291; 1F18.
DR GO: 0004263; F:chymotrypsin activity; IEA.
DR GO: 0008233; F:peptidase activity; IEA.
DR GO: 0004295; F:trypsin activity; IEA.
DR GO: 0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR001254; Peptidase_S1.
DR InterPro: IPR001314; Peptidase_S1A.
DR InterPro: IPR009003; Pept_Ser_Cys.
DR Pfam: PF00089; Trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PROSITE: PS0240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 254 AA; 27682 MW; CA13F453FAP45192 CRC64;

Query Match
Best Local Similarity 56.1%; Score 639.5; DB 2; Length 254;
Matches 121; Conservative 33; Mismatches 64; Indels 3; Gaps 1;

QY 1 IVGGRARPHAWPMVSLQRLGCGATLIAPNFVMSAAHCVANVNVRAVRVVLGA 57
DB 1 IVGGRARPHAWPMVSLQRLGCGATLIAPNFVMSAAHCVANVNVRAVRVVLGA 57
QY 30 IVGGRARPHAWPMVSLQRLGCGATLIAPNFVMSAAHCVANVNVRAVRVVLGA 89
DB 30 IVGGRARPHAWPMVSLQRLGCGATLIAPNFVMSAAHCVANVNVRAVRVVLGA 89
QY 58 HNLRSRREPTQVAVORIFENGDPVNLNDIVILQNGSATINANVQVAPLPAQGRRLG 117
DB 58 HNLRSRREPTQVAVORIFENGDPVNLNDIVILQNGSATINANVQVAPLPAQGRRLG 117

Db 90 HDLLSEPEQOKFTITQVFENNYPETLNDVLLQLNRPASLGKQVAVASLPQDQSL 149
QY 118 NGVQCLAMGGLGRNGRIASVLOELNVVTSLSLRRSNVCTLVGRGAGVCFGDSGPL 177
DB 150 QGTQCLAMGGLGRNGRIASVLOELNVVTSLSLRRSNVCTLVGRGAGVCFGDSGPL 209
QY 178 VCNGLIHGIASFVRCGACSLGYPADAFAPVAFQVFNWIDSIQ 218
DB 210 ICNGLIHGVSFVIRECASLQFPDFARVSMYVNIHSLR 250

RESULT 8
ID PRN3_HUMAN STANDARD; PRT; 256 AA.
AC P24158; P15637; P18078; Q9U0D8;
DC 01-APR-1990 (Rel. 14, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Myeloblastin precursor (EC 3.4.21.76) (Leukocyte proteinase 3) (PR-3)
DE (PR3) (AGP7) (Wegener's autoantigen) (P29) (C-ANCA antigen)
DE (Neutrophil proteinase 4) (NP-4).
GN Name=PRN3; Synonyms=MBN;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SQ SEQUENCE FROM N.A.
RA MEDLINE=92021028; PubMed=1681549;
RA Labbaye C., Musette P., Cayre Y.E.;
RT "Wegener autoantigen and myeloblastin are encoded by a single mRNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:9253-9256(1991).
RN [2]
SQ SEQUENCE FROM N.A.
RA PubMed=15057824; DOI=10.1038/nature02399;
RA Grimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J.,
RA Lamerdin J.E., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M.,
RA Aerts A., Altherr M., Ashworth L., Bajorek E., Black S., Branscomb E.,
RA Caenepeel S., Carrano A.V., Caolice C., Chan Y.M., Christensen M.,
RA Cleland C.A., Copeland A., Dallin E., Dehal P., Denys M., Dettler J.C.,
RA Escobar J., Flowers D., Fotopoulos D., Garcia C., Georgescu A.M.,
RA Glavina T., Gomez M., Gonzales E., Groza N., Hammon N., Hawkins T.,
RA Haydu L., Ho I., Huang W., Israni S., Jett J., Kadner K., Kimball H.,
RA Kobayashi A., Larionov V., Leem S.-H., Lopez P., Lou Y., Lowry S.,
RA Malfatti S., Martinez D., McCready P.M., Medina C., Morgan J.,
RA Nelson K., Nolan M., Ovcharenko I., Pitluck S., Pollard M.,
RA Popkie A.P., Predki P., Quan G., Ramirez L., Rash S., Retterer J.,
RA Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D.,
RA Slezak T., Solovyev V., Thayer N., Tice H., Tsai M., Ustaszewska A.,
RA Vo N., Wagner M., Wheeler J., Wu K., Xie G., Yang J., Dubchak I.,
RA Furey T.S., DeJong P., Dickson M., Gordon D., Eichler E.E.,
RA Pennacchio L.A., Richardson P., Stubbs L., Rokhsar D.S., Myers R.M.,
RA Rubin E.M., Lucas S.M.;
RT "The DNA sequence and biology of human chromosome 19.";
RL Nature 428:529-535(2004).
RN [3]
SQ SEQUENCE OF 2-256 FROM N.A., AND SEQUENCE OF 48-71 AND 156-181.
RA MEDLINE=91079774; PubMed=2258701;
RA Campanelli D., Melchior M., Fu Y., Nakata M., Shuman H., Nathan C.,
RA Gabay J.E.;
RT "Cloning of cDNA for proteinase 3: a serine protease, antibiotic, and
RT autoantigen from human neutrophils.";
RL J. Exp. Med. 172:1709-1715(1990).
RN [4]
SQ SEQUENCE OF 1-20 AND 22-256 FROM N.A.
RA MEDLINE=92390417; PubMed=1518849;
RA Zimmer M., Medcalf R.L., Fink T.M., Mattmann C., Lichter P.,
RA Jenne D.E.;
RT "Three human elastase-like genes coordinately expressed in the
RT myelomonocyte lineage are organized as a single genetic locus on
RT 19pter.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:8215-8219(1992).

```


between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC

[5] SEQUENCE OF 1-200 FROM N.A., AND VARIANT ILE-119.
 MEDLINE=99123768; PubMed=994693;
 CC Clave E., Mollard J., Hensel N., Rapis A., Barrett A.J.;
 RA "Donor-recipient polymorphism of the proteinase 3 gene: a potential
 RT target for T-cell alloresponses to myeloid leukemia.";
 RL J. Immunother. 22:1-6(1999).
 CC [6]
 RN SEQUENCE OF 42-256 FROM N.A.
 RP MEDLINE=90090622; PubMed=2598267; DOI=10.1016/0092-8674(99)90752-6;
 RX Borjes D., Raynal M.-C., Solomon D.H., Darzynkiewicz Z., Cayre Y.E.;
 RA "Down-regulation of a serine protease, myeloblastin, causes growth
 RT arrest and differentiation of promyelocytic leukemia cells.";
 RL Cell 59:959-968(1989).
 CC [7]
 RN SEQUENCE OF 28-67 AND 228-244.
 RP MEDLINE=91236723; PubMed=2033050;
 RX Rao N.V., Wehner N.G., Marshall B.C., Gray W.R., Gray B.H.,
 RA Hoidal J.R.;
 RA "Characterization of proteinase-3 (PR-3), a neutrophil serine
 RT proteinase. Structural and functional properties.";
 RL J. Biol. Chem. 266:9540-9548(1991).
 CC [8]
 RN SEQUENCE OF 28-52.
 RP MEDLINE=91025622; PubMed=2121162;
 RX Ohlsson K., Linder C., Rosengren M.;
 RA "Monoclonal antibodies specific for neutrophil proteinase 4.
 RT Production and use for isolation of the enzyme.";
 RL Biol. Chem. Hoppe-Seyler 371:549-555(1990).
 CC [9]
 RN SEQUENCE OF 28-47.
 RP MEDLINE=89315847; PubMed=2501794;
 RX Gabay J.E., Scott R.W., Campanelli D., Griffith J., Wilde C.,
 RA Marra M.N., Seeger M., Nathan C.F.;
 RA "Antibiotic proteins of human polymorphonuclear leukocytes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:5610-5614(1989).
 CC [10]
 RN SEQUENCE OF 28-47 AND 196-219.
 RP MEDLINE=90130450; PubMed=2404977;
 RX Wilde C.G., Snable J.L., Griffith J.E., Scott R.W.;
 RA "Characterization of two azurophilic granule proteases with active-site
 RT homology to neutrophil elastase.";
 RL J. Biol. Chem. 265:2038-2041(1990).
 CC [11]
 RN SEQUENCE OF 28-48, AND IDENTITY OF WEGENER'S AUTOANTIGEN WITH PR-3.
 RP MEDLINE=9032035; PubMed=2377228; DOI=10.1038/346520a0;
 RX Jenne D.E., Tschopp J., Luedemann J., Utecht B., Gross W.L.;
 RA "Wegener's autoantigen decoded.";
 RL Nature 346:520-520(1990).
 CC [12]
 RN IDENTITY OF WEGENER'S AUTOANTIGEN WITH PROTEINASE 3.
 RP MEDLINE=91055123; PubMed=2242436;
 RX Gupta S.K., Niles J.L., McCluskey R.T., Arnaut M.A.;
 RA "Identity of Wegener's autoantigen (p29) with proteinase 3 and
 RT myeloblastin.";
 RL Blood 76:2162-2162(1990).
 CC [13]
 RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RP MEDLINE=96346178; PubMed=8757293; DOI=10.1006/jmbi.1996.0458;
 RX Fujinaga M., Charnia M.M., Halenbeck R., Koths K., James M.N.G.;
 RA "The crystal structure of PR3, a neutrophil serine proteinase antigen
 RT of Wegener's granulomatosis antibodies.";
 RL J. Mol. Biol. 261:267-278(1996).
 CC -1- FUNCTION: Polymorphonuclear leukocyte serine protease that
 CC degrades elastin, fibronectin, laminin, vitronectin, and collagen
 CC types I, III, and IV (in vitro) and causes emphysema when
 CC administered by tracheal insufflation to hamsters.
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of proteins, including elastin, by
 CC preferential cleavage: Ala-Xaa > Val-Xaa.
 CC -1- SIMILARITY: Belongs to the peptidase S1 family. Elastase
 CC subfamily.
 CC

This SWISS-PROT entry is copyright. It is produced through a collaboration

EMBL; X56132; CAA39598.1; --
 DR EMBL; AC004799; -- NOT ANNOTATED_CDS.
 DR EMBL; M75154; AAA59558.1; --
 DR EMBL; M96839; AAB59493.1; --
 DR EMBL; M96838; AAB59493.1; JOINED.
 DR EMBL; M96837; AAB59493.1; JOINED.
 DR EMBL; X55668; CAA39203.1; --
 DR EMBL; M29142; AAA36342.1; --
 DR EMBL; AF015449; AAD21524.1; --
 DR EMBL; AF015446; AAD21524.1; JOINED.
 DR EMBL; AF015447; AAD21524.1; JOINED.
 DR EMBL; AF015448; AAD21524.1; JOINED.
 DR EMBL; M96628; AAB59364.1; --
 DR PIR; A45080; PRHU3.
 DR PDB; 1FUJ; X-ray; A/B/C/D=28-248.
 DR MEROPS; S01.134; --
 DR Genew; HGNC:9495; PRN3.
 DR MIM; 177020; --
 DR GO; GO:0008236; F:serine-type peptidase activity; NAS.
 DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
 DR InterPro; IPR009003; Pept_Ser_Cys.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00089; Trypsin_1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM0020; TRYP_SPC; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW 3D-structure; Collagen degradation; Direct protein sequencing;
 KW Glycoprotein; Hydrolase; Polymorphism; Serine protease; Signal;
 KW Zymogen.
 FT SIGNAL 1 25
 FT PROPEP 26 27
 FT CHAIN 28 248
 FT PROPEP 249 256
 FT ACT_SITE 71 71
 FT ACT_SITE 118 118
 FT ACT_SITE 203 203
 FT CARBOHYD 129 129
 FT CARBOHYD 174 174
 FT DISULFID 56 72
 FT DISULFID 152 209
 FT DISULFID 182 188
 FT DISULFID 199 224
 FT VARIANT 119 119
 FT VARIANT 135 135
 FT VARIANT 136 136
 FT VARIANT 136 136
 FT CONFLICT 2 2
 FT CONFLICT 46 46
 FT CONFLICT 48 48
 FT CONFLICT 64 64
 FT CONFLICT 70 70
 FT CONFLICT 255 255
 FT STRAND 29 29
 FT STRAND 32 33
 FT TURN 36 37
 FT TURN 40 41
 Myeloblastin.
 Charge relay system.
 Charge relay system.
 Charge relay system.
 N-linked (GlcNAc...) (Potential).
 N-linked (GlcNAc...)
 V -> I (in dbSNP:351111).
 A -> T (in dbSNP:1042281).
 T -> S (in dbSNP:1042282).
 FTID=VAR 011691.
 FTID=VAR 011713.
 FTID=VAR 011714.
 A -> R (in Ref. 3).
 Q -> E (in Ref. 9 and 10).
 R -> A (in Ref. 8).
 S -> D (in Ref. 7).
 A -> P (in Ref. 1).
 Missing (in Ref. 3).

Query Match 56.0%; Score 638.5; DB 1; Length 256;
 Best Local Similarity 54.1%; Pred. No. 1.2e-49;
 Matches 120; Conservative 41; Mismatches 58; Indels 3; Gaps 1;

```
QY 1 IVGGRARPHAMFPMVLSQLR---GGHFCGATLIAPNFVMSAAHCVANVNVRAVRVVLGA 57
DB 28 IVGGHEAQPHSRPYMASLQWRGNPGSHFGCGTLIHPSFVLTAHCLRDIPQRLVNVVLGA 87
QY 58 HNLSREPTQVFAVORIFENGTDPNVLLNDIVILQNGSATINNVQVQLPAQCRRLG 117
DB 88 HNVRTQEPHQHFSVAQVFLNNYDAENKLVLLIQLSSPANLSASVATVQLPQQDQVP 147
QY 118 NGVQCLAMGWLGRNRGSIASVLQELNVTVTSLCRSSNVCTLVGRQAGVCFGDSGSP 177
DB 148 HGTOCLAMGWRGVGAHDPPAQVQLQELNVTVTFFCRPHNICTFVPRKAGICFGDSGGPL 207
QY 178 VCNGLIHGTASVPRGCGASGLYPDAPAPVAQFVNWIDSIIOR 219
DB 208 ICDGIIQIGDSFVINGCATRLFPDFTRVALYVDWIRSTLR 249
```

RESULT 9

```
Q6LBN2 PRELIMINARY; PRT; 237 AA.
AC Q6LBN2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Proteinase 3 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=90332035; PubMed=2377228; DOI=10.1038/346520a0;
RA Jenne D.E., Teichmann J., Ludemann J., Utecht B., Gross W.L.;
RT "Wegener's autoantigen decoded.";
RL Nature 346:520-520 (1990).
RN [2]
RP SEQUENCE FROM N.A.
RA Jenne D.;
RL Submitted (OCT-1990) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; X56132; CAA39597.1; -.
DR HSSP; P20160; 1A7S.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease; Signal.
FT NON_TER 1 1
FT SIGNAL <1 6 Potential.
FT CHAIN 9 237 Potential.
SQ SEQUENCE 237 AA; 25884 MW; 38ECA16F6BCD292 CRC64;
```

```
Query Match 55.9%; Score 637.5; DB 2; Length 237;
Best Local Similarity 54.5%; Pred. NO. 1.4e-49;
Matches 121; Conservative 40; Mismatches 58; Indels 3; Gaps 1;
```

```
QY 1 IVGGRARPHAMFPMVLSQLR---GGHFCGATLIAPNFVMSAAHCVANVNVRAVRVVLGA 57
DB 9 IVGGHEAQPHSRPYMASLQWRGNPGSHFGCGTLIHPSFVLTAHCLRDIPQRLVNVVLGA 68
QY 58 HNLSREPTQVFAVORIFENGTDPNVLLNDIVILQNGSATINNVQVQLPAQCRRLG 117
DB 69 HNVRTQEPHQHFSVAQVFLNNYDAENKLVLLIQLSSPANLSASVATVQLPQQDQVP 128
```

```
QY 118 NGVQCLAMGWLGRNRGSIASVLQELNVTVTSLCRSSNVCTLVGRQAGVCFGDSGSP 177
DB 129 HGTOCLAMGWRGVGAHDPPAQVQLQELNVTVTFFCRPHNICTFVPRKAGICFGDSGGPL 188
QY 178 VCNGLIHGTASVPRGCGASGLYPDAPAPVAQFVNWIDSIIOR 219
DB 189 ICDGIIQIGDSFVINGCATRLFPDFTRVALYVDWIRSTLR 230

RESULT 10
PRN3_MOUSE STANDARD; PRT; 254 AA.
AC Q61096; O08809;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Myeloblastin precursor (EC 3.4.21.76) (Proteinase 3) (PR-3).
GN Name=PrtN3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RX MEDLINE=99126347; PubMed=9925946;
RA Sturrock A., Franklin K.P., Wu S.-Q., Hoidal J.R.;
RT "Characterization and localization of the genes for mouse proteinase-3 (PrtN3) and neutrophil elastase (Ela2).";
RL Cytogenet. Cell Genet. 83:104-108(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RX MEDLINE=97330929; PubMed=9187364; DOI=10.1016/S0014-5793(97)00418-3;
RA Jenne D.E., Froehlich L., Hummel A.M., Specks U.;
RT "Cloning and functional expression of the murine homologue of proteinase 3: implications for the design of murine models of RT vasculitis.";
RL FEBS Lett. 408:187-190(1997).
RN [3]
RP SEQUENCE OF 2-254 FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=97362044; PubMed=9211743; DOI=10.1007/s002510050260;
RA Aveskogh M., Lutzelschwab C., Huang M.R., Hellman L.;
RT "Characterization of cDNA clones encoding mouse proteinase 3 (myeloblastin) and cathepsin G.";
RL Immunogenetics 46:181-191(1997).
CC -!- FUNCTION: Polymorphonuclear leukocyte serine protease that degrades elastin, fibronectin, laminin, vitronectin, and collagen types I, III, and IV (in vitro) and causes emphysema when administered by tracheal insufflation to hamsters (By similarity).
CC -!- CATALYTIC ACTIVITY: Hydrolysis of proteins, including elastin, by preferential cleavage: Ala-Xaa > Val-Xaa.
CC -!- SIMILARITY: Belongs to the peptidase S1 family. Elastase subfamily.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC
DR EMBL; AF082186; AAC79701.1; -.
DR EMBL; U97073; AAB58055.1; -.
DR EMBL; U45325; AAB67271.1; -.
DR HSSP; P18291; 1F18.
DR MEROPS; S01.134; -.
DR MGD; MGI:891580; Prtn3.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
```

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzinski M.I., Skalska U., Smalish D.E., Schmerch A., Schein J.E.,
RA Jones S.J., Marra M.A.,
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.",
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Whole body;
RC Klein S., Gerhard D.S.;
RE Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
RL -1- SIMILARITY: Belongs to peptidase family S1.
CC EMBL; BC076933; AAH76933.1; -
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin_1;
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOW_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Hydrolase; Protease; Serine protease.
KW HYDROLASE; PROTEASE; SERINE PROTEASE.
SQ SEQUENCE 245 AA; 26530 MW; B982EA7CA4613EF2 CRC64;

Query Match 50.8%; Score 579.5; DB 2; Length 245;
Best Local Similarity 52.3%; Pred. No. 2.6e-44; Indels 1; Gaps 1;
Matches 114; Conservative 33; Mismatches 70;

QY 1 IVGGRRAPHPMPVSLQLR--GGHFCGATLIAPNFVMSAAHCVANNVRAVRVVLGA 60
DB 26 IVGGREATPNHPYATLSQLRHFCCGSLIAPQFLMTAAHCVANNVRAVRVVLGA 85

QY 61 SRREPTQVAVQRIFFENGTPDVLNDIVILQNGSATINNAVQALPAQGRRLNGV 120
DB 86 RANETKQRFVQVFNQFENGFPDLTQNDIVILKLDPRVSLNGKQVQVSLPANEVPA 145

QY 121 QCLANGWGLLGRNGIASVLQELNVTVV-TSLCRSSNVCTLVRGQAGVCFGDSGPLV 179
DB 146 QCVTAGWGRSLSTEGQIPRLQELNVTVVTRQNLCPENNICTGVFMQAGICFGDSGPLV 205

QY 180 NGLIHGIASFVRGCGASGLYPDAFAPVQFVNWIDSII 217
DB 206 NGVIQGITSFIRSCGNGVTPDFFSRVSIFRFDIDAI 243

RESULT 12
CAP7 HUMAN STANDARD; PRT; 251 AA.
ID CAP7_HUMAN
AC P20150; P80014;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Azurocidin precursor (Cationic antimicrobial protein CAP37) (Heparin-
DE binding protein) (HBP).
GN Name=AZU1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92013155; PubMed=1919011;
RA Morgan J.G., Sukienicki T., Pereira H.A., Spitznagel J.K.,
RA Guerra M.E., Larrick J.L.;
RA "Cloning of the cDNA for the serine protease homolog CAP37/azurocidin,
RT

DR Pfam; PF00089; Trypsin; 1.
DR SMART; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Collagen degradation; Glycoprotein; Hydrolase; Serine protease;
KW Signal; Zymogen.
FT SIGNAL 1 27 By similarity.
FT PROPEP 28 29 By similarity.
FT CHAIN 30 250 Myeloblastin.
FT PROPEP 251 254 By similarity.
FT ACT_SITE 73 73 Charge relay system (By similarity).
FT ACT_SITE 120 120 Charge relay system (By similarity).
FT ACT_SITE 205 205 Charge relay system (By similarity).
FT CARBOHYD 127 127 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 176 176 N-linked (GlcNAc...) (Potential).
FT DISULFID 58 74 By similarity.
FT DISULFID 154 211 By similarity.
FT DISULFID 184 190 By similarity.
FT DISULFID 201 226 By similarity.
FT CONFLICT 2 2 S -> A (in Ref. 2).
SQ SEQUENCE 254 AA; 27626 MW; 00CB989A3CB79CA CRC64;

Query Match 55.7%; Score 635.5; DB 1; Length 254;
Best Local Similarity 53.8%; Pred. No. 2.3e-49; Indels 3; Gaps 1;
Matches 119; Conservative 37; Mismatches 62;

QY 1 IVGGRRAPHPMPVSLQLR--GGHFCGATLIAPNFVMSAAHCVANNVRAVRVVLGA 57
DB 30 IVGGREATPNHPYATLSQLRHFCCGSLIAPQFLMTAAHCVANNVRAVRVVLGA 89

QY 58 HNLRRPTQVAVQRIFFENGTPDVLNDIVILQNGSATINNAVQALPAQGRRLNG 117
DB 90 HDLLSSPEQKFTISQVFNQVFNPEENLDVLLQLNRTASLGKEVAVASLPQQDTLS 149

QY 118 NGVQCLANGWGLLGRNGIASVLQELNVTVV-TSLCRSSNVCTLVRGQAGVCFGDSGPL 177
DB 150 QGTQCLANGWGRSLSTEGQIPRLQELNVTVVTRQNLCPENNICTGVFMQAGICFGDSGPL 209

QY 178 VCNGLIHGIASFVRGCGASGLYPDAFAPVQFVNWIDSII 218
DB 210 ICNGILHGVDSFVIRECASLQFPDFARVSMYVDVIQNLVR 250

RESULT 11
Q6DF10 PRELIMINARY; PRT; 245 AA.
AC Q6DF10;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Fla2-prov protein.
GN Name=fla2-prov;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole body;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RT a microbicidal and chemotactic protein from human granulocytes.";
RL J. Immunol. 147:3210-3214(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92390417; PubMed=1518849;
RA Zimmer M., Medcalf R.L., Fink T.M., Mattmann C., Lichter P.,
RA Jenne D.E.;
RT "Three human elastase-like genes coordinately expressed in the
RT myelomonocyte lineage are organized as a single genetic locus on
RT 19pter.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:8215-8219(1992).
RN [3]
RP SEQUENCE FROM N.A.
RX PubMed=15057824; DOI=10.1038/nature02399;
RA Grimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J.,
RA Lamerdin J.E., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M.,
RA Aerts A., Altherr M., Ashworth L., Bajorek E., Black S., Branscomb E.,
RA Caenepeel S., Carrano A.V., Caoile C., Chan Y.M., Christensen M.,
RA Cleland C.A., Copeland A., Dalling E., Dehal P., Denys M., Dettler J.C.,
RA Escobar J., Flowers D., Fotopoulos D., Garcia C., Georgescu A.M.,
RA Glavina T., Gomez M., Gonzales E., Groza M., Hammon N., Hawkins T.,
RA Haydu L., Ho I., Huang W., Israni S., Jett J., Kadner K., Kimball H.,
RA Kobayashi A., Lartionov V., Leem S.-H., Lopez P., Lou Y., Lowry S.,
RA Malfatti S., Martinez D., McCreedy P.M., Medina C., Morgan J.,
RA Nelson K., Nolan M., Ovcharenko I., Pitluck S., Pollard M.,
RA Popkie A.P., Predki P., Quan G., Ramirez L., Rash S., Retterer J.,
RA Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D.,
RA Slezak T., Solovyev V., Thayer N., Tice H., Tsai M., Ustaszewska A.,
RA Vo N., Wagner M., Wheeler J., Wu K., Xie G., Yang J., Dubchak I.,
RA Furey T.S., DeJong P., Dickson M., Gordon D., Eichler E.E.,
RA Pennacchio L.A., Richardson P., Stubbs L., Rokhsar D.S., Myers R.M.,
RA Rubin E.M., Lucas S.M.;
RT "The DNA sequence and biology of human chromosome 19.";
RL Nature 428:529-535(2004).
RN [4]
RP SEQUENCE OF 3-251 FROM N.A.
RC TISSUE=Neutrophils;
RX MEDLINE=91264832; PubMed=2049091;
RA Almeida R.P., Melchior M., Campanelli D., Nathan C., Gabay J.E.;
RT "Complementary DNA sequence of human neutrophil azurocidin, an
RT antibiotic with extensive homology to serine proteases.";
RL Biochem. Biophys. Res. Commun. 177:688-695(1991).
RN [5]
RP SEQUENCE OF 27-248.
RX MEDLINE=91032128; PubMed=2226832; DOI=10.1016/0014-5793(90)80484-Z;
RA Pohl J., Pereira H.A., Martin N.M., Spitznagel J.K.;
RT "Amino acid sequence of CAP37, a human neutrophil granule-derived
RT antibacterial and monocyte-specific chemotactic glycoprotein
RT structurally similar to neutrophil elastase.";
RL FEBS Lett. 272:200-204(1990).
RN [6]
RP SEQUENCE OF 27-248.
RC TISSUE=Neutrophils;
RX MEDLINE=91224149; PubMed=2026172;
RA Floodgaard H., Oestergaard E., Bayne S., Svendsen A., Thomsen J.,
RA Engels M., Wollmer A.;
RT "Covalent structure of two novel neutrophil leucocyte-derived
RT proteins of porcine and human origin. Neutrophil elastase homologues
RT with strong monocyte and fibroblast chemotactic activities.";
RL Eur. J. Biochem. 197:535-547(1991).
RN [7]
RP SEQUENCE OF 27-47.
RX MEDLINE=91378304; PubMed=1897955;
RA Green B.G., Weston H., Ashe B.M., Doherty J., Finke P., Hagmann W.,
RA Lark M., Mao J., Maycock A., Moore V., Mumford R., Shah S.,
RA Walakavits L., Knight W.B.;
RT "FMN elastases: a comparison of the specificity of human isozymes and
RT the enzyme from other species toward substrates and inhibitors.";
RL Arch. Biochem. Biophys. 286:284-292(1991).
RN [8]
RP SEQUENCE OF 27-46.
RX MEDLINE=89315847; PubMed=2501794;
RA Gabay J.E., Scott R.W., Campanelli D., Griffith J., Wilde C.,
Marra M.N., Seeger M., Nathan C.F.;
RT "Antibiotic proteins of human polymorphonuclear leukocytes.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:5610-5614(1989).
RN [9]
RP SEQUENCE OF 27-46 AND 194-217.
RX MEDLINE=90130450; PubMed=2404977;
RA Wilde C.G., Snable J.L., Griffith J.E., Scott R.W.;
RT "Characterization of two azurophil granule proteases with active-site
RT homology to neutrophil elastase.";
RL J. Biol. Chem. 265:2038-2041(1990).
RN [10]
RP SEQUENCE OF 27-67.
RC TISSUE=Neutrophils;
RX MEDLINE=90157837; PubMed=2406527; DOI=10.1016/0024-3205(90)90104-Y;
RA Pereira H.A., Spitznagel J.K., Pohl J., Wilson D.E., Morgan J.,
RA Palling I., Larrick J.W.;
RT "CAP 37, a 37 kD human neutrophil granule cationic protein shares
RT homology with inflammatory proteinases.";
RL Life Sci. 46:189-196(1990).
RN [11]
RP SEQUENCE OF 27-68.
RC TISSUE=Neutrophils;
RX MEDLINE=90237224; PubMed=2332502;
RA Pereira H.A., Shafer W.M., Pohl J., Martin L.E., Spitznagel J.K.;
RT "CAP37, a human neutrophil-derived chemotactic factor with monocyte
RT specific activity.";
RL J. Clin. Invest. 85:1468-1476(1990).
RN [12]
RP REVIEW.
RX MEDLINE=92095171; PubMed=1755383;
RA Morgan J.G., Pereira H.A., Sukienicki T., Spitznagel J.K.,
RA Larrick J.W.;
RT "Human neutrophil granule cationic protein CAP37 is a specific
RT macrophage chemotaxin that shares homology with inflammatory
RT proteinases.";
RL Adv. Exp. Med. Biol. 305:89-96(1991).
RN [13]
RP SYNTHESIS OF 46-70.
RX MEDLINE=93281653; PubMed=8506327;
RA Pereira H.A., Erdem I., Pohl J., Spitznagel J.K.;
RT "Synthetic bactericidal peptide based on CAP37: a 37-kDa human
RT neutrophil granule-associated cationic antimicrobial protein
RT chemotactic for monocytes.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:4733-4737(1993).
RN [14]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RX MEDLINE=97249288; PubMed=9095193;
RA Iversen L.F., Kastrup J.S., Bjoern S.E., Rasmussen P.B., Wiberg F.C.,
RA Floodgaard H.J., Larsen I.K.;
RT "Structure of HBP, a multifunctional protein with a serine proteinase
RT fold.";
RL Nat. Struct. Biol. 4:265-268(1997).
RN [15]
RP X-RAY CRYSTALLOGRAPHY (1.12 ANGSTROMS).
RX MEDLINE=98437573; PubMed=9761855; DOI=10.1107/S0907444997016193;
RA Karlsson S., Iversen L.F., Larsen I.K., Floodgaard H.J., Kastrup J.S.;
RT "Atomic resolution structure of human HBP/CAP37/azurocidin.";
RL Acta Crystallogr. D 54:598-609(1998).
RN [16]
RP FUNCTION: This is a neutrophil granule-derived antibacterial and
RP monocyte- and fibroblast-specific chemotactic glycoprotein. Binds
RP heparin. The cytotoxic action is limited to many species of Gram-
RP negative bacteria; this specificity may be explained by a strong
RP affinity of the very basic N-terminal half for the negatively
RP charged lipopolysaccharides that are unique to the Gram-negative
RP bacterial outer envelope. It may play a role in mediating
RP recruitment of monocytes in the second wave of inflammation.
RN [17]
RP SUBUNIT: Monomer.
RN [18]
RP SUBCELLULAR LOCATION: Cytoplasmic granules of neutrophils.
RN [19]
RP SIMILARITY: Belongs to the peptidase S1 family. Elastase
RN subfamily.
RN [20]
RP This SWISS-PROT entry is copyright. It is produced through a collaboration
RP between the Swiss Institute of Bioinformatics and the EMBL outstation -

the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announcement/>) or send an email to license@isb-sib.ch.

EMBL: M96326; AAB59353.1; -
EMBL: X58794; CAA41601.1; -
EMBL: AC004799; -; NOT_ANNOTATED_CDS.
PIR: A46268; TRHUZ.

PDB: 1A7S; X-ray; @=27-251.
PDB: 1AB5; X-ray; @=27-250.
PDB: 1FX1; X-ray; A=27-250.
PDB: 1FX3; X-ray; A=27-250.
MEROPS; S01.971; -
GEM; HGNC:913; AZU1.
MIM; 162815; -

GO: 0042582; C:azurophil granule; IDA.
GO: 0005576; C:extracellular; NAS.
GO: 0008201; F:heparin binding; NAS.
GO: 0015643; F:toxin binding; NAS.
GO: 0045123; P:cellular extravasation; NAS.
GO: 0050829; P:defense response to Gram-negative bacteria; TAS.
GO: 0008347; P:glia cell migration; IDA.
GO: 0050930; P:induction of caspase activation; NAS.
GO: 0001719; P:inhibition of caspase activation; NAS.
GO: 0048246; P:macrophage chemotaxis; NAS.
GO: 0001774; P:macrogial cell activation; IEP.
GO: 0042117; P:monocyte activation; TAS.
GO: 0045785; P:positive regulation of cell adhesion; IDA.
GO: 0050754; P:positive regulation of fractalkine biosynth. . ; IDA.
GO: 0050725; P:positive regulation of interleukin-1 beta b. . ; IDA.
GO: 0045348; P:positive regulation of MHC class II biosynt. . ; IEP.
GO: 0050766; P:positive regulation of phagocytosis; IDA.
GO: 0042535; P:positive regulation of tumor necrosis facto. . ; IDA.
GO: 0007205; P:protein kinase C activation; TAS.

Query Match 42.1%; Score 480; DB 1; Length 251;
Best Local Similarity 45.2%; Pred. No. 2.7e-35;
Matches 99; Conservative 35; Mismatches 81; Indels 4; Gaps 3;

QY 1 IVGRRARPHAWPMVSLQRLGGHFCGATLIAPNFVMSAAHCNVANVNRVVLGAHNL 60
DB 27 IVGRRARPHAWPMVSLQRLGGHFCGATLIAPNFVMSAAHCNVANVNRVVLGAHNL 86
QY 61 SRRE-PTQVFAVQIFENGTPDVLNLDIVILQNGSATINANVOVAQLPAQGRRLGNG 119
DB 87 RRRERQSRQTFSISSMSNGYDPOQNLNDMLLDREANLTSVTLPLPLQNAVTEAG 146
QY 120 VCLAMGGLLRNGRIASVLQELNVTVV-TSLCRSNVCTLVGRQAGVCFDGSGLPLV 178
DB 147 TRCVAGWSQSRGSLRFRFFVNVTVTPEDQCRPNVCTGVLTGRGICNGDGGTPLV 206
QY 179 CNGLIHGTFVGGCAGSLYDPDAPFAVQFVNWIDSII 217
DB 207 CEGLAGVASFSLGCGRG--PDFETVALFRDWIDGVL 243

RESULT 13
CAP7_PIG STANDARD; PRT; 219 AA.
ID AC P80015;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Aurocidin (Cationic antimicrobial protein CAP37) (Heparin-binding protein) (HBP).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.

RC TISSUE=Neutrophils;
RX MEDLINE=91224149; PubMed=2026172;
RA Flodgaard H., Oestergaard E., Bayne S., Svendsen A., Thomsen J.,
RA Engelst M., Wollmer A.;
RT "Covalent structure of two novel neutrophil leucocyte-derived
RT proteins of porcine and human origin. Neutrophil elastase homologues
RT with strong monocyte and fibroblast chemotactic activities.";
RL Eur. J. Biochem. 197;535-547(1991).
RN [2]

RP PARTIAL SEQUENCE, DISULFIDE BONDS, CARBOHYDRATE-LINKAGE SITES ASN-113
RP AND ASN-144, AND MASS SPECTROMETRY.
RX PubMed=2076469;
RA Sorensen H.H., Thomsen J., Bayne S., Højrup P., Roepstorff P.;
RA "Strategies for determination of disulphide bridges in proteins using
RT plasma desorption mass spectrometry.";
RL Biomed. Environ. Mass Spectrom. 19;713-720(1990).
CC -!- FUNCTION: This is a neutrophil granule-derived antibacterial and
CC monocyte- and fibroblast-specific chemotactic glycoprotein. Binds
CC heparin.

CC -!- SUBUNIT: Monomer.
CC -!- SIMILARITY: Belongs to the peptidase S1 family. Elastase
CC subfamily.
CC PIR: S15393; TRPGAZ.
DR HSRPS; P20160; IAT5.
DR MERPS; S01.971; -

DR GO: 0042582; C:azurophil granule; ISS.
DR GO: 0005576; C:extracellular; ISS.
DR GO: 0008201; F:heparin binding; ISS.
DR GO: 0015643; F:toxin binding; ISS.
DR GO: 0045123; P:cellular extravasation; ISS.
DR GO: 0050829; P:defense response to Gram-negative bacteria; ISS.
DR GO: 0008347; P:glia cell migration; ISS.
DR GO: 0050930; P:induction of positive chemotaxis; ISS.
DR GO: 0001719; P:inhibition of caspase activation; ISS.
DR GO: 0048246; P:macrophage chemotaxis; ISS.
DR GO: 0001774; P:macrogial cell activation; ISS.
DR GO: 0042117; P:monocyte activation; ISS.
DR GO: 0045785; P:positive regulation of cell adhesion; ISS.
DR GO: 0050754; P:positive regulation of fractalkine biosynth. . ; ISS.
DR GO: 0050725; P:positive regulation of interleukin-1 beta b. . ; ISS.
DR GO: 0045348; P:positive regulation of MHC class II biosynt. . ; ISS.

DR GO: 0050766; P:positive regulation of phagocytosis; ISS.
DR GO: 0042535; P:positive regulation of tumor necrosis facto. . ; ISS.
DR GO: 0007205; P:protein kinase C activation; ISS.
DR InterPro; IPR009003; Pept Ser Cys.
DR InterPro; IPR01254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1a.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYD_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; FALSE_NEG.
DR PROSITE; PS00135; TRYPSIN_SER; FALSE_NEG.
DR Antibiotic; Chemotaxis; Direct protein sequencing; Glycoprotein;
KW Heparin-binding; Serine protease homolog.
FT CARBOHYD 113 113 N-linked (GlcNAc. . .).
FT CARBOHYD 144 144 N-linked (GlcNAc. . .).
FT DISULFID 26 42
FT DISULFID 122 179
FT DISULFID 152 158
SQ SEQUENCE 219 AA; 24301 MW; 99129CAD880749D CRC64;

Query Match 37.5%; Score 428; DB 1; Length 219;
Best Local Similarity 41.1%; Pred. No. 1.2e-30;
Matches 90; Conservative 40; Mismatches 83; Indels 6; Gaps 2;

QY 1 IVGRRARPHAWPMVSLQRLGGHFCGATLIAPNFVMSAAHCNVANVNRVVLGAHNL 60
DB 1 IVGRRARPHAWPMVSLQRLGGHFCGATLIAPNFVMSAAHCNVANVNRVVLGAHNL 60
QY 61 SRREPTQVFAVQIFENGTPDVLNLDIVILQNGSATINANVOVAQLPAQGRRLGNGV 120
DB 61 RQEQSRQTFSIRSIQNGYDPRQNLNDVLLQDLREARLTTPSVALVPLPQNAVTEAGT 120

RESULT 15

Q6GYP5	ID	Q6GYP5	PRELIMINARY;	PRT;	264 AA.
AC	06GYP5;				
AT	05-JUL-2004	(TrEMBLrel. 27, Created)			
DT	05-JUL-2004	(TrEMBLrel. 27, Last sequence update)			
DT	05-JUL-2004	(TrEMBLrel. 27, Last annotation update)			
DE	LOC398300 protein.				
GN	Names=LOC398300;				
OS	Xenopus laevis (African clawed frog).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;				
OC	Xenopodinae; Xenopus.				
OX	NCBI_TaxID=8355;				
OX	[1]				
RP	SEQUENCE FROM N.A.				
RP	TTSSUE=Spleen;				
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;				
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,				
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA	Scapletoen L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Scapletoen M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,				
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,				
RA	Bosak A.A., McGowan J.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,				
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Rabey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,				
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,				
RA	Krzywinski M.I., Skalska U., Smaltus D.E., Schnerch A., Schein J.E.,				
RA	Jones S.J., Marra M.A.;				
RT	"Generation and initial analysis of more than 15,000 full-length human				
RT	and mouse cDNA sequences."				
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).				
RL	[2]				
RP	SEQUENCE FROM N.A.				
RP	TTSSUE=Spleen;				
RC	MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;				
RX	Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,				
RA	Richardson P.;				
RT	"Genetic and genomic tools for Xenopus research: The NIH Xenopus				
RT	initiative."				
RL	Dev. Dyn. 225:384-391 (2002).				
RL	[3]				
RP	SEQUENCE FROM N.A.				
RP	TTSSUE=Spleen;				
RC	Klein S., Strausberg R.;				
RX	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.				
CC	-1- SIMILARITY: belongs to peptidase family S1.				
CC	EMBL; BC072970; AAH72970.1; "				
DR	GO; GO:0004263; F:chymotrypsin activity; IEA.				
DR	GO; GO:0008233; F:peptidase activity; IEA.				
DR	GO; GO:0004295; F:trypsin activity; IEA.				
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.				
DR	InterPro; IPR001254; Peptidase S1.				
DR	InterPro; IPR001314; Peptidase S1A.				
DR	InterPro; IPR009003; Pept_Ser_Cys.				
DR	Pfam; PF00089; Trypsin; 1				
DR	PRINTS; PR00722; CHYMOTRYPSIN.				
DR	SMART; SM00020; TRY SP; 1.				
DR	PROSITE; PS00240; TRYPSIN_DOM; 1.				
DR	PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.				
DR	PROSITE; PS00135; TRYPSIN_SER; 1.				
KW	Hydrolase; Protease; Serine protease.				
SEQUENCE	264 AA; 28066 MW; 1AD1FD9CB43C1A53 CRC64;				

Query Match 34.2%; Score 390; DB 2; Length 264;
Best Local Similarity 38.8%; Pred. No. 4e-27;

us-10-733-288a-4.rup

Mon Apr 18 13:05:50 2005

Matches		94; Conservative	41; Mismatches	77; Indels	30; Gaps	10;
QY	1	IVGGRARRPHAPFVMSLQLRGG----	HFCGATLIAPNFVMSAAHCVANVVRV--	RVV	54	
Db	28	VIGGSEASRNSWFWQISLQYSSSGSWYHTCGGSLIRANRVMTAAHCVD----	RAVSRYRV	83		
QY	55	LGAHNLSRREPTROVFAVORIFENGTFDVLNLLN--	DIVILQLNGSATINANVQVQLPA	111		
Db	84	VGDNHYQNDGTEQYISVSRIVKHANWPNNTAGGYDIAVLHLASSATLNSYVKLAQLPA	143			
QY	112	QGRRLNGVQCCLAMGWGLLGRNRGIASVLQELNVTVT-----	SLCRBSNVCTL	160		
Db	144	DGAVLGHNYNCVVTGWGKTSNNGNLASALQOAPLPVVAHATCSSGSGYWGSTVKSTMVCAG	203			
QY	161	VRGRQAGVCEGDSGPLVC--NGL--IHGIASFV-RGGCAGLYPDAPAPVAQFVNWIDS	215			
Db	204	GDGVRSG-CQGDGGPLNCPVNGVYQVHGVTSFVSSSGCSTYLKPTVTRVSAIYIGWINN	262			
QY	216	II	217			
Db	263	NI	264			

Search completed: April 18, 2005, 12:49:24
Job time : 181 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 18, 2005, 12:49:34 ; Search time 135 Seconds
(without alignments)
539.179 Million cell updates/sec

Title: US-10-733-288A-4
Perfect score: 1140
Sequence: 1 IVGRRARPHAMFVMSLQI.....PDAPFVQFVNMDSIIOR 219

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1421835 seqs, 332370683 residues
Total number of hits satisfying chosen parameters: 1421835

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTU5_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1133	99.4	238	11	US-09-789-210-31
2	1133	99.4	238	16	US-10-408-765A-197
3	1123	98.5	218	16	US-10-408-765A-87
4	1114	97.7	218	9	US-09-861-708-3
5	632.5	55.5	229	11	US-09-789-210-30
6	480	42.1	222	15	US-10-423-311-1
7	480	42.1	225	11	US-09-789-210-32
8	480	42.1	225	17	US-10-868-577A-30
9	480	42.1	251	17	US-10-868-577A-38
10	416	36.5	199	14	US-10-384-474-8
11	414	36.3	199	15	US-10-423-311-2
12	376	33.0	284	9	US-09-888-615-112
13	372	32.6	283	10	US-09-946-374-111

14	372	32.6	283	13	US-10-052-586-272	Sequence 272, App
15	372	32.6	283	14	US-10-174-590-272	Sequence 272, App
16	372	32.6	283	14	US-10-176-758-272	Sequence 272, App
17	372	32.6	283	14	US-10-175-737-272	Sequence 272, App
18	372	32.6	283	14	US-10-174-581-272	Sequence 272, App
19	372	32.6	283	14	US-10-176-481-272	Sequence 272, App
20	372	32.6	283	14	US-10-176-749-272	Sequence 272, App
21	372	32.6	283	14	US-10-176-914-272	Sequence 272, App
22	372	32.6	283	14	US-10-176-915-272	Sequence 272, App
23	372	32.6	283	14	US-10-173-706-272	Sequence 272, App
24	372	32.6	283	14	US-10-175-738-272	Sequence 272, App
25	372	32.6	283	14	US-10-175-752-272	Sequence 272, App
26	372	32.6	283	14	US-10-176-482-272	Sequence 272, App
27	372	32.6	283	14	US-10-176-757-272	Sequence 272, App
28	372	32.6	283	14	US-10-176-913-272	Sequence 272, App
29	372	32.6	283	14	US-10-180-552-272	Sequence 272, App
30	372	32.6	283	14	US-10-180-557-272	Sequence 272, App
31	372	32.6	283	14	US-10-173-700-272	Sequence 272, App
32	372	32.6	283	14	US-10-175-740-272	Sequence 272, App
33	372	32.6	283	14	US-10-174-579-272	Sequence 272, App
34	372	32.6	283	14	US-10-174-582-272	Sequence 272, App
35	372	32.6	283	14	US-10-174-588-272	Sequence 272, App
36	372	32.6	283	14	US-10-175-739-272	Sequence 272, App
37	372	32.6	283	14	US-10-175-743-272	Sequence 272, App
38	372	32.6	283	14	US-10-176-488-272	Sequence 272, App
39	372	32.6	283	14	US-10-176-492-272	Sequence 272, App
40	372	32.6	283	14	US-10-176-747-272	Sequence 272, App
41	372	32.6	283	14	US-10-176-750-272	Sequence 272, App
42	372	32.6	283	14	US-10-176-985-272	Sequence 272, App
43	372	32.6	283	14	US-10-176-987-272	Sequence 272, App
44	372	32.6	283	14	US-10-176-992-272	Sequence 272, App
45	372	32.6	283	14	US-10-176-992-272	Sequence 272, App

ALIGNMENTS

RESULT 1
US-09-789-210-31
; Sequence 31, Application US/09789210
; Publication No. US20040241646A1
; GENERAL INFORMATION:
; APPLICANT: COHEN, MAURICE
; COLPITTS, TRACEY L.
; FRIEDMAN, PAULA N.
; GRANADOS, EDWARD N.
; KLASS, MICHAEL R.
; RUSSELL, JOHN C.
; STEWART, KENT D.
; STROUPE, STEVEN D.
; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
; AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
; OF THE PROSTATE
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/789,210
; FILING DATE: 20-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/944,483
; FILING DATE: <Unknown>

ug-10-733-288a-4.rapb

Mon Apr 18 13:05:49 2005

[illegible]

```

RESULT 3
US-10-408-765A-87
; Sequence 87, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 87
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-408-765A-87

```

RESULT 4
US-09-861-708-3
; Sequence 3, Application US/09861708
; Patent No. US20020098188A1
; GENERAL INFORMATION:
; APPLICANT: KAIBARA, Makoto
; APPLICANT: IWATA, Hioki
; APPLICANT: TAKIO, Koji
; APPLICANT: DOHMAE, Naoshi
; TITLE OF INVENTION: Blood Coagulation Factor-Activating Protein and Antibody Thereof
; FILE REFERENCE: P21011
; CURRENT APPLICATION NUMBER: US/09/861,708
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: JP 153096/2000
; PRIOR FILING DATE: 2000-05-24

```

ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 238 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: None
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-09-789-210-31

Query Match          99.4%; Score 1133; DB 11; Length 238;
Best Local Similarity 99.5%; Pred. No. 6.9e-110;
Matches 218; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  IVGRRARPHAPPMVSLQRLRGHFCGATLIIAPNFWMSAAHCVANNVRAVRVVLGAHNL 60
Db      1  IVGRRARPHAPPMVSLQRLRGHFCGATLIIAPNFWMSAAHCVANNVRAVRVVLGAHNL 60
QY      61  SRRPETRQVFAVQIFENGSTDPVNNLLNDIVILQLNGSATINANVOAQLPAQGRRLNGV 120
Db      61  SRRPETRQVFAVQIFENGSTDPVNNLLNDIVILQLNGSATINANVOAQLPAQGRRLNGV 120
QY      121  QCLANGWGLLGRNRGIASVLOELNVTVTSLCRSRNVCTLVRGROAGVCFDGSGLPVCN 180
Db      121  QCLANGWGLLGRNRGIASVLOELNVTVTSLCRSRNVCTLVRGROAGVCFDGSGLPVCN 180
QY      181  GLIHGIIASFVRGGCASGLYPDAFAPVAQFVNWIDSIQIR 219
Db      181  GLIHGIIASFVRGGCASGLYPDAFAPVAQFVNWIDSIQIR 219

```

RESULT 2
US-10-408-765A-197
; Sequence 197, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 197
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-197

120

; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; TYPE: PRT
; LENGTH: 218
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (218)..(218)
; OTHER INFORMATION: Unknown Amino Acid
US-09-861-708-3

Query Match 97.7%; Score 1114; DB 9; Length 218;
Best Local Similarity 99.1%; Pred. No. 6e-108;
Matches 215; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 IVGRRARPHAWPFMVSQLRGCGATLIAFNFMVMSAAHCVANNVRAVRVVLGAHNL 60
DB 1 IVGRRARPHAWPFMVSQLRGCGATLIAFNFMVMSAAHCVANNVRAVRVVLGAHNL 60
QY 61 SRREPTQVFAVQRIFFENGDPVNLNDIVILQNGSATINANVQVAQLPAQGRRLNGV 120
DB 61 SRREPTQVFAVQRIFFENGDPVNLNDIVILQNGSATINANVQVAQLPAQGRRLNGV 120
QY 121 QCLAMGWLGRNREGIASVLQELNVTVTSLCRSSNVCTLVGRQAGVCFDGSGLVCN 180
DB 121 QCLAMGWLGRNREGIASVLQELNVTVTSLCRSSNVCTLVGRQAGVCFDGSGLVCN 180
QY 181 GLIHGIASFVRGCGASGLYPDAFAPVAQFVNWIDSII 217
DB 181 GLIHGIASFVRGCGASGLYPDAFAPVAQFVNWIDSII 217

RESULT 5
US-09-789-210-30
; Sequence 30, Application US/09789210
; Publication No. US20040241646A1
; GENERAL INFORMATION:
; APPLICANT: COHEN, MAURICE
; COLPITTS, TRACEY L.
; FRIEDMAN, PAULA N.
; GRANADOS, EDWARD N.
; KLASS, MICHAEL R.
; RUSSELL, JOHN C.
; STEWART, KENT D.
; STROUPE, STEVEN D.
; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
; AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
; OF THE PROSTATE
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/789,210
; FILING DATE: 20-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/944,483
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6183. US. 01

TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 229 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: None
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-789-210-30

Query Match 55.5%; Score 632.5; DB 11; Length 229;
Best Local Similarity 54.1%; Pred. No. 1.2e-57;
Matches 120; Conservative 40; Mismatches 59; Indels 3; Gaps 1;

QY 1 IVGRRARPHAWPFMVSQLR--GGHFCGATLIAFNFMVMSAAHCVANNVRAVRVVLGA 57
DB 1 IVGGHEAQPSPRYMASLQMRGNPGSHFCGTLIHPSFVLTAHCLRDIPQRLVNVVLGA 60
QY 58 HNLSRREPTQVFAVQRIFFENGDPVNLNDIVILQNGSATINANVQVAQLPAQGRRLG 117
DB 61 HNVRTQEPQQHFSVAQVFLNNYDAENKNDILLIQLSSPAMLSASVTSVQLPQQQPPV 120
QY 118 NGVQCLAMGWLGRNREGIASVLQELNVTVTSLCRSSNVCTLVGRQAGVCFDGSGL 177
DB 121 HGTQCLAMGWRGVGAHDPPAQVLQELNVTVTFFCFRPHNICTFVPRKAGICFGDGGPL 180
QY 178 VCNGLIHGIASFVRGCGASGLYPDAFAPVAQFVNWIDSIIQR 219
DB 181 ICDGIITQIDSFVWGCAIRLPDPDFRVALYVDWIRSLRR 222

RESULT 6
US-10-423-311-1
; Sequence 1, Application US/10423311
; Publication No. US20030206938A1
; GENERAL INFORMATION:
; APPLICANT: Pereira, Heloise Anne
; APPLICANT: Chodosh, James
; APPLICANT: Callegan, Michelle C.
; TITLE OF INVENTION: TREATMENT AND INHIBITION OF OCULAR INFECTIONS AND WOUNDS BY CAP37
; TITLE OF INVENTION: CAP37 PEPTIDES
; FILE REFERENCE: 6267.002
; CURRENT APPLICATION NUMBER: US/10/423,311
; CURRENT FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: 60/378,295
; PRIOR FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-423-311-1

Query Match 42.1%; Score 480; DB 15; Length 222;
Best Local Similarity 45.2%; Pred. No. 1e-41;
Matches 99; Conservative 35; Mismatches 81; Indels 4; Gaps 3;

QY 1 IVGRRARPHAWPFMVSQLRGCGATLIAFNFMVMSAAHCVANNVRAVRVVLGAHNL 60
DB 1 IVGRRARPHAWPFMVSQLRGCGATLIAFNFMVMSAAHCVANNVRAVRVVLGAHNL 60
QY 61 SRRE-PTQVFAVQRIFFENGDPVNLNDIVILQNGSATINANVQVAQLPAQGRRLNG 119
DB 61 RRRRQSRQTSISSSENSGYDPPQNLNDMLQLDREANLTSSVITLPLQNAIVEAG 120
QY 120 VOCLAMGWLGRNREGIASVLQELNVTVV-TSICRSNVCTLVGRQAGVCFDGSGLV 178
DB 121 TRCQVAGWGSQSGGLSRFPFNVTVTPEDQCRPNNVCTGVLTTRRGICNGDGGTPLV 180

Db 121 TRCOVAGSGRSGRLSRFPFVNVTVPEDQCRNNVCTGLTRRGTCNGDGTPLV 180
Qy 179 CNGLIHGIAFVRGGCASGLYPDAFAPVAQFVNWIDSII 217
Db 181 CEGLAHGVASFSLGPCGRG--PDFFTRVALFRDWIDGVL 217

RESULT 8
US-10-868-577A-30
; Sequence 30, Application US/10868577A
; Publication No. US20050032697A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al.
; TITLE OF INVENTION: HEPARIN BINDING VEGFR-3 LIGANDS
; FILE REFERENCE: 28967/39359A
; CURRENT APPLICATION NUMBER: US/10/868,577A
; CURRENT FILING DATE: 2004-06-14
; PRIOR APPLICATION NUMBER: US 60/478,390
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: US 10/669,176
; PRIOR FILING DATE: 2003-09-23
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 30
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-868-577A-30

Query Match 42.1%; Score 480; DB 17; Length 225;
Best Local Similarity 45.2%; Pred. No. 1e-41;
Matches 99; Conservative 35; Mismatches 81; Indels 4; Gaps 3;
Qy 1 IVGGRARPHAPFVMSLQLRGHCFCGATLIAPNFVMSAAHCVANVVRVVLGAHNL 60
Db 1 IVGGRARPHAPFVMSLQLRGHCFCGATLIAPNFVMSAAHCVANVVRVVLGAHNL 60
Qy 61 SRRE-PTQVFAVQRIFFENGTDPNLLNDIVILQNGSATINANVQVQLPAQGRRLNG 119
Db 61 RRRRSQRTFTSISSMSGYDPOQNLNDMLLDREANLTSSVTILPLQNAIVEAG 120
Qy 120 VQCLAMGWLLGNRGIASVLQELNVTVV-TSLCRSNVCTLVGRQAGVCFDGSGLV 178
Db 121 TRCOVAGSGRSGRLSRFPFVNVTVPEDQCRNNVCTGLTRRGTCNGDGTPLV 180
Qy 179 CNGLIHGIAFVRGGCASGLYPDAFAPVAQFVNWIDSII 217
Db 181 CEGLAHGVASFSLGPCGRG--PDFFTRVALFRDWIDGVL 217

RESULT 9
US-10-868-577A-38
; Sequence 38, Application US/10868577A
; Publication No. US20050032697A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al.
; TITLE OF INVENTION: HEPARIN BINDING VEGFR-3 LIGANDS
; FILE REFERENCE: 28967/39359A
; CURRENT APPLICATION NUMBER: US/10/868,577A
; CURRENT FILING DATE: 2004-06-14
; PRIOR APPLICATION NUMBER: US 60/478,390
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: US 10/669,176
; PRIOR FILING DATE: 2003-09-23
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 38
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-868-577A-38

Qy 179 CNGLIHGIAFVRGGCASGLYPDAFAPVAQFVNWIDSII 217
Db 181 CEGLAHGVASFSLGPCGRG--PDFFTRVALFRDWIDGVL 217
RESULT 7
US-09-789-210-32
; Sequence 32, Application US/09789210
; Publication No. US20040241646A1
; GENERAL INFORMATION:
; APPLICANT: COHEN, MAURICE
; COLPITTS, TRACEY L.
; FRIEDMAN, PAULA N.
; GRANADOS, EDWARD N.
; KLASS, MICHAEL R.
; RUSSELL, JOHN C.
; STEWART, KENT D.
; STROUPE, STEVEN D.
; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
; AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
; OF THE PROSTATE
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/789,210
; FILING DATE: 20-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/944,483
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6183.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: None
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:

US-09-789-210-32
Query Match 42.1%; Score 480; DB 11; Length 225;
Best Local Similarity 45.2%; Pred. No. 1e-41;
Matches 99; Conservative 35; Mismatches 81; Indels 4; Gaps 3;
Qy 1 IVGGRARPHAPFVMSLQLRGHCFCGATLIAPNFVMSAAHCVANVVRVVLGAHNL 60
Db 1 IVGGRARPHAPFVMSLQLRGHCFCGATLIAPNFVMSAAHCVANVVRVVLGAHNL 60
Qy 61 SRRE-PTQVFAVQRIFFENGTDPNLLNDIVILQNGSATINANVQVQLPAQGRRLNG 119
Db 61 RRRRSQRTFTSISSMSGYDPOQNLNDMLLDREANLTSSVTILPLQNAIVEAG 120
Qy 120 VQCLAMGWLLGNRGIASVLQELNVTVV-TSLCRSNVCTLVGRQAGVCFDGSGLV 178

Query Match 42.1%; Score 480; DB 17; Length 251;
Best Local Similarity 45.2%; Pred. No. 1.2e-41;
Matches 99; Conservative 35; Mismatches 81; Indels 4; Gaps 3;
QY 1 IVGGRARPHAWPFVMSLQGRGHFCGATLIAPNFVMSAAHCVANVRAVRVVLGAHNL 60
DB 27 IVGGRARPHAWPFVMSLQGRGHFCGATLIAPNFVMSAAHCVANVRAVRVVLGAHNL 86
QY 61 SRREPTRQVFAVORIFEN-GTDPVNLNDIVILQNGSATINANVQVLAQPAQGRRLGNG 119
DB 87 RRRERQSRQTFSSISSMSSENGYDPOQNLNDMLLDREANLTSSVTILPLQNAATVEAG 146
QY 120 VQCLAMGWLGNRNGIASVLQELNVTIV-TSLCRSNVCTLVGRQAGVCFDGSPLV 178
DB 147 TRCOVAGWGSQRSGRLSPFPFVNVTVPEDQCRPNNVCTGLTRRGICNGDGGTPLV 206
QY 179 CNLGHGASVFRVGGCASGLYPDAFAPVAQFVNWIDSII 217
DB 207 CEGLAHGVAASFSLGPCRG--PDFTRVALFRDWIDGVL 243
RESULT 10
US-10-384-474-8
; Sequence 8, Application US/10384474
; Publication No. US20030170745A1
; GENERAL INFORMATION:
; APPLICANT: Pereira, Heloise Anne
; TITLE OF INVENTION: AN EARLY DETECTION MARKER FOR CHRONIC INFLAMMATORY ASSOCIATED DIS
; FILE REFERENCE: 6267.001
; CURRENT APPLICATION NUMBER: US/10/384,474
; CURRENT FILING DATE: 2003-03-07
; PRIOR FILING DATE: 2002-03-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-384-474-8
Query Match 36.5%; Score 416; DB 14; Length 199;
Best Local Similarity 43.8%; Pred. No. 4.3e-35;
Matches 88; Conservative 31; Mismatches 78; Indels 4; Gaps 3;
QY 19 QLRGHHFCGATLIAPNFVMSAAHCVANVRAVRVVLGAHNL-SRRE-PTROVFAVORIFE 77
DB 1 QNGRHFCCGALIHARFVMTAASCFOQNPQGVSTVILGAYDLRRERQSRQTFSSISMS 60
QY 78 NGTDPVNLNDIVILQNGSATINANVQVLAQPAQGRRLGNGVQCLAMGWLGNRNGIA 137
DB 61 NGYDPOQNLNDMLLDREANLTSSVTILPLQNAATVEAGTRCQVAGWGSQRSGRLS 120
QY 138 SVLQELNVTIV-TSLCRSNVCTLVGRQAGVCFDGSPLVNCGLIHGIASVFRVGGCAS 196
DB 121 RPFVNVTVPEDQCRPNNVCTGLTRRGICNGDGGTPLVCEGLAHGVAASFSLGPCRG 180
QY 197 GLYPDAFAPVAQFVNWIDSII 217
DB 181 G--PDFTRVALFRDWIDGVL 199
RESULT 11
US-10-423-311-2
; Sequence 2, Application US/10423311
; Publication No. US20030206938A1
; GENERAL INFORMATION:
; APPLICANT: Pereira, Heloise Anne
; APPLICANT: Chodosh, James
; APPLICANT: Callegan, Michelle C.
; TITLE OF INVENTION: TREATMENT AND INHIBITION OF OCULAR INFECTIONS AND WOUNDS BY CAP37
; FILE REFERENCE: 6267.002

; CURRENT APPLICATION NUMBER: US/10/423,311
; CURRENT FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: 60/378,295
; PRIOR FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-423-311-2

Query Match 36.3%; Score 414; DB 15; Length 199;
Best Local Similarity 43.7%; Pred. No. 6.9e-35;
Matches 87; Conservative 31; Mismatches 77; Indels 4; Gaps 3;
QY 21 RCGHFCGATLIAPNFVMSAAHCVANVRAVRVVLGAHNL-SRRE-PTROVFAVORIFENG 79
DB 2 QGRHFCCGALIHARFVMTAASCFOQNPQGVSTVILGAYDLRRERQSRQTFSSISMSSENG 61
QY 80 TDPVNLNDIVILQNGSATINANVQVLAQPAQGRRLGNGVQCLAMGWLGNRNGIASV 139
DB 62 YDPQNLNDMLLDREANLTSSVTILPLQNAATVEAGTRCQVAGWGSQRSGRLSRF 121
QY 140 LQELNVTIV-TSLCRSNVCTLVGRQAGVCFDGSPLVNCGLIHGIASVFRVGGCASGL 198
DB 122 RPFVNVTVPEDQCRPNNVCTGLTRRGICNGDGGTPLVCEGLAHGVAASFSLGPCRG- 180
QY 199 YPDAPAPVAQFVNWIDSII 217
DB 181 -PDFTRVALFRDWIDGVL 198

RESULT 12
US-09-888-615-112
; Sequence 112, Application US/09888615
; Patent No. US20020064858A1
; GENERAL INFORMATION:
; APPLICANT: FLOWMAN, GREGORY
; APPLICANT: WHYTE, DAVID
; APPLICANT: CAENEPEL, SEAN
; APPLICANT: CHASYDCZAK, GLEN
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/09/888,615
; CURRENT FILING DATE: 2001-06-26
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 112
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-888-615-112

Query Match 33.0%; Score 376; DB 9; Length 284;
Best Local Similarity 36.6%; Pred. No. 1e-30;
Matches 87; Conservative 32; Mismatches 93; Indels 26; Gaps 5;
QY 1 IVGGRARPHAWPFVMSLQGRGHFCGATLIAPNFVMSAAHCVANVRAVRVVLGAHNL 60
DB 35 IIGGHEVTPHSPRYMASVFRGQHCGGFLLRARVWVSAACHCFSHRDLRTGLVVLGAHVL 94
QY 61 SRREPTRQVFAVORIFEN-GTDPVNLNDIVILQNGSATINANVQVLAQPAQGRRL- 116
DB 95 STAEPTQQVFGIDALTTPDYPHMTHANDICLLQNGSAVLGPAVGLLRLP--GRRARPP 152
QY 117 GNGVQCLAMGWLGNRNGIASVLQELNVTIV-----VTSLCRSNVCTLV 161
DB 153 TAGTRCRVAGWGFVSDFEELPGLMEAKVRVLDPPVCNNSWKHGLTILMLCTRSG----- 207

Mon Apr 18 13:05:49 2005

us-10-733-288a-4.rapb

QY 162 RRGAGVCFDGSPLVCLNGLIHGIAFVRGCGASGLYDPAFAPVAQFVNNWIDSIOR 219
 Db 208 DSHRRGFCGADSGPLVCRNRAHGLVFSGLWCGDPKTPDVTQVSAFVAWIWDVVR 265

RESULT 13

US-09-946-374-111
 ; Sequence 111, Application US/09946374
 ; Publication No. US20030073129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2830P1C1
 ; CURRENT APPLICATION NUMBER: US/09/946,374
 ; CURRENT FILING DATE: 2001-09-04
 ; PRIOR APPLICATION NUMBER: 60/098716
 ; PRIOR FILING DATE: 1998-09-01
 ; PRIOR APPLICATION NUMBER: 60/098723
 ; PRIOR FILING DATE: 1998-09-01
 ; PRIOR APPLICATION NUMBER: 60/098749
 ; PRIOR FILING DATE: 1998-09-01
 ; PRIOR APPLICATION NUMBER: 60/098750
 ; PRIOR FILING DATE: 1998-09-01
 ; PRIOR APPLICATION NUMBER: 60/098803
 ; PRIOR FILING DATE: 1998-09-02
 ; PRIOR APPLICATION NUMBER: 60/098821
 ; PRIOR FILING DATE: 1998-09-02
 ; PRIOR APPLICATION NUMBER: 60/098843
 ; PRIOR FILING DATE: 1998-09-02
 ; PRIOR APPLICATION NUMBER: 60/098536
 ; PRIOR FILING DATE: 1998-09-09
 ; PRIOR APPLICATION NUMBER: 60/099596
 ; PRIOR FILING DATE: 1998-09-09
 ; PRIOR APPLICATION NUMBER: 60/099598
 ; PRIOR FILING DATE: 1998-09-09
 ; PRIOR APPLICATION NUMBER: 60/099602
 ; PRIOR FILING DATE: 1998-09-09
 ; PRIOR APPLICATION NUMBER: 60/099642
 ; PRIOR FILING DATE: 1998-09-09
 ; PRIOR APPLICATION NUMBER: 60/099741
 ; PRIOR FILING DATE: 1998-09-10
 ; PRIOR APPLICATION NUMBER: 60/099754
 ; PRIOR FILING DATE: 1998-09-10
 ; PRIOR APPLICATION NUMBER: 60/099763
 ; PRIOR FILING DATE: 1998-09-10
 ; PRIOR APPLICATION NUMBER: 60/099792
 ; PRIOR FILING DATE: 1998-09-10
 ; PRIOR APPLICATION NUMBER: 60/099808
 ; PRIOR FILING DATE: 1998-09-10
 ; PRIOR APPLICATION NUMBER: 60/099812
 ; PRIOR FILING DATE: 1998-09-10
 ; PRIOR APPLICATION NUMBER: 60/099815
 ; PRIOR FILING DATE: 1998-09-10
 ; PRIOR APPLICATION NUMBER: 60/099816
 ; PRIOR FILING DATE: 1998-09-10
 ; PRIOR APPLICATION NUMBER: 60/100385
 ; PRIOR FILING DATE: 1998-09-15
 ; PRIOR APPLICATION NUMBER: 60/100388
 ; PRIOR FILING DATE: 1998-09-15
 ; PRIOR APPLICATION NUMBER: 60/100390
 ; PRIOR FILING DATE: 1998-09-15
 ; PRIOR APPLICATION NUMBER: 60/100584
 ; PRIOR FILING DATE: 1998-09-16
 ; PRIOR APPLICATION NUMBER: 60/100627
 ; PRIOR FILING DATE: 1998-09-16
 ; PRIOR APPLICATION NUMBER: 60/100661
 ; PRIOR FILING DATE: 1998-09-16
 ; PRIOR APPLICATION NUMBER: 60/100662
 ; PRIOR FILING DATE: 1998-09-16
 ; PRIOR APPLICATION NUMBER: 60/100664
 ; PRIOR FILING DATE: 1998-09-16
 ; PRIOR APPLICATION NUMBER: 60/100683
 ; PRIOR FILING DATE: 1998-09-17
 ; PRIOR APPLICATION NUMBER: 60/100684
 ; PRIOR FILING DATE: 1998-09-17
 ; PRIOR APPLICATION NUMBER: 60/100710
 ; PRIOR FILING DATE: 1998-09-17
 ; PRIOR APPLICATION NUMBER: 60/100711
 ; PRIOR FILING DATE: 1998-09-17
 ; PRIOR APPLICATION NUMBER: 60/100848
 ; PRIOR FILING DATE: 1998-09-18
 ; PRIOR APPLICATION NUMBER: 60/100849
 ; PRIOR FILING DATE: 1998-09-18
 ; PRIOR APPLICATION NUMBER: 60/100919
 ; PRIOR FILING DATE: 1998-09-17
 ; PRIOR APPLICATION NUMBER: 60/100930
 ; PRIOR FILING DATE: 1998-09-17
 ; PRIOR APPLICATION NUMBER: 60/101014
 ; PRIOR FILING DATE: 1998-09-18
 ; PRIOR APPLICATION NUMBER: 60/101068
 ; PRIOR FILING DATE: 1998-09-18
 ; PRIOR APPLICATION NUMBER: 60/101071
 ; PRIOR FILING DATE: 1998-09-18
 ; PRIOR APPLICATION NUMBER: 60/101279
 ; PRIOR FILING DATE: 1998-09-22
 ; PRIOR APPLICATION NUMBER: 60/101471
 ; PRIOR FILING DATE: 1998-09-23
 ; PRIOR APPLICATION NUMBER: 60/101472
 ; PRIOR FILING DATE: 1998-09-23
 ; PRIOR APPLICATION NUMBER: 60/101474
 ; PRIOR FILING DATE: 1998-09-23
 ; PRIOR APPLICATION NUMBER: 60/101475
 ; PRIOR FILING DATE: 1998-09-23
 ; PRIOR APPLICATION NUMBER: 60/101476
 ; PRIOR FILING DATE: 1998-09-23
 ; PRIOR APPLICATION NUMBER: 60/101477
 ; PRIOR FILING DATE: 1998-09-23
 ; PRIOR APPLICATION NUMBER: 60/101479
 ; PRIOR FILING DATE: 1998-09-23
 ; PRIOR APPLICATION NUMBER: 60/101738
 ; PRIOR FILING DATE: 1998-09-24
 ; PRIOR APPLICATION NUMBER: 60/101741
 ; PRIOR FILING DATE: 1998-09-24
 ; PRIOR APPLICATION NUMBER: 60/101743
 ; PRIOR FILING DATE: 1998-09-24
 ; PRIOR APPLICATION NUMBER: 60/101915
 ; PRIOR FILING DATE: 1998-09-24
 ; PRIOR APPLICATION NUMBER: 60/101916
 ; PRIOR FILING DATE: 1998-09-24
 ; PRIOR APPLICATION NUMBER: 60/102207
 ; PRIOR FILING DATE: 1998-09-29
 ; PRIOR APPLICATION NUMBER: 60/102240
 ; PRIOR FILING DATE: 1998-09-29
 ; PRIOR APPLICATION NUMBER: 60/102307

		Query Match	32.6%;	Score 372;	DB 10;	Length 283;	
		Best Local Similarity	36.1%;	Pred. No. 2.6e-30;			
		Matches	86;	Conservative	33;	Mismatches	93;
						Indels	26; Gaps
							5;
QY	1	I VCGRRARPHAWPFWLSQLRLRGGHFCATLIAPNFMVMSAAHCVANVRVAVVLGAHNL	60				
		: : : : : : : : : : : : : : : :					
Dd	34	IUGHEVTPHSRPYMASVRGQHCCGGFLRARRWVSAAKCFSHRDRTGLVLVGHAHL	93				
		: : : : : : : : : : : : : : : :					
QY	61	SREPTQRFVAQRIFEN-GTDPVNLLNDIVILQLNGSATINANVVQAQLPAQGRL---	116				
		: : : : : : : : : : : : : : : :					

Mon Apr 18 13:05:49 2005

;; PRIOR FILING DATE: 1997-12-18
;; PRIOR APPLICATION NUMBER: 60/077450
;; PRIOR FILING DATE: 1998-03-10
;; PRIOR APPLICATION NUMBER: 60/077632
;; PRIOR FILING DATE: 1998-03-11
;; PRIOR APPLICATION NUMBER: 60/077649
;; PRIOR FILING DATE: 1998-03-11
;; PRIOR APPLICATION NUMBER: 60/078886
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/078939
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/079664
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/079786
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/080107
;; PRIOR FILING DATE: 1998-03-31
;; PRIOR APPLICATION NUMBER: 60/080194
;; PRIOR FILING DATE: 1998-03-31
;; PRIOR APPLICATION NUMBER: 60/080327
;; PRIOR FILING DATE: 1998-04-01
;; PRIOR APPLICATION NUMBER: 60/080333
;; PRIOR FILING DATE: 1998-04-01
;; PRIOR APPLICATION NUMBER: 60/081049
;; PRIOR FILING DATE: 1998-04-08
;; PRIOR APPLICATION NUMBER: 60/081070
;; PRIOR FILING DATE: 1998-04-08
;; PRIOR APPLICATION NUMBER: 60/081195
;; PRIOR FILING DATE: 1998-04-09
;; PRIOR APPLICATION NUMBER: 60/081838
;; PRIOR FILING DATE: 1998-04-15
;; PRIOR APPLICATION NUMBER: 60/082568
;; PRIOR FILING DATE: 1998-04-21
;; PRIOR APPLICATION NUMBER: 60/082569
;; PRIOR FILING DATE: 1998-04-21
;; PRIOR APPLICATION NUMBER: 60/082704
;; PRIOR FILING DATE: 1998-04-22
;; PRIOR APPLICATION NUMBER: 60/082797
;; PRIOR FILING DATE: 1998-04-22
;; PRIOR APPLICATION NUMBER: 60/083322
;; PRIOR FILING DATE: 1998-04-28
;; PRIOR APPLICATION NUMBER: 60/083495
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083496
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083499
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083559
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/084366
;; PRIOR FILING DATE: 1998-05-05
;; PRIOR APPLICATION NUMBER: 60/084414
;; PRIOR FILING DATE: 1998-05-06
;; PRIOR APPLICATION NUMBER: 60/084639
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084640
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084643
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085579
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085580
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085582
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085700
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/086023
;; PRIOR FILING DATE: 1998-05-18
;; PRIOR APPLICATION NUMBER: 60/086392
;; PRIOR FILING DATE: 1998-05-22

;; PRIOR APPLICATION NUMBER: 60/086486
;; PRIOR FILING DATE: 1998-05-22
;; PRIOR APPLICATION NUMBER: 60/087098
;; PRIOR FILING DATE: 1998-05-28
;; PRIOR APPLICATION NUMBER: 60/087208
;; PRIOR FILING DATE: 1998-05-28
;; PRIOR APPLICATION NUMBER: 60/087609
;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/087759
;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/087827
;; PRIOR FILING DATE: 1998-06-03
;; PRIOR APPLICATION NUMBER: 60/088025
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088028
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088029
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088033
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088167
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088202
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088212
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088217
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088326
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088655
;; PRIOR FILING DATE: 1998-06-09
;; PRIOR APPLICATION NUMBER: 60/088722
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088738
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088740
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088811
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088824
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088825
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088826
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088861
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/088863
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/088876
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/089090
;; PRIOR FILING DATE: 1998-06-12
;; PRIOR APPLICATION NUMBER: 60/089105
;; PRIOR FILING DATE: 1998-06-12
;; PRIOR APPLICATION NUMBER: 60/089512
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089514
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089538
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089598
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089653
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089908

Query Match 32.6%; Score 372; DB 13; Length 283;
Best Local Similarity 36.1%; Pred. No. 2.6e-30;
Matches 86; Conservative 33; Mismatches 93; Indels 26; Gaps 5;

Qy 1 IVGRRARPHANFPMVSLQURGGHFCGATLIAFNFMVSAHCVANNVRAVRVVLGAHNL 60

Db 34 IIGHEVTPHSRPMASVREGGQHCGFLRLARWVVSAAHCFSHRDLRTGLVVLGAHVL 93
Qy 61 SREPTQVFAVQRIEEN-CTDPVNLNDIVILQNGSATINANVOVAQLPAQGRRL--- 116
Db 94 STAEPTQVFGIDALTTHPDYHPMTHANDICLLRLNGSAVLGPAVGLLRPL--GRRARPP 151
Qy 117 GNGVQCLAMGWLGRNRGIASVLQELNVTV-----VTSLCRRSNVCTLV 161
Db 152 TAGTRCRVAGWGFVSDPEELPPGLMEAKVRVLDPDVCNSSWGHLTLTLMCTRSRSG----- 206
Qy 162 RGRQAGVCFGDSGLVNCGLIHGIASFVRGGCASGLYPDAPAPVAQFVNWIDSIIQR 219
Db 207 DSHRRGFCSDSGPLVCRNRAHGLVSFSLWCWGDPKTPDVTYQVSAFVAWIWDVVRR 264

RESULT 15
US-10-174-590-272
; Sequence 272, Application US/10174590
; Publication No. US20030008352A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C42
; CURRENT APPLICATION NUMBER: US/10/174,590
; CURRENT FILING DATE: 2002-06-18
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 272
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-174-590-272

Query Match 32.6%; Score 372; DB 14; Length 283;
Best Local Similarity 36.1%; Pred. No. 2, 6e-30;
Matches 86; Conservative 33; Mismatches 93; Indels 26; Gaps 5;
Qy 1 IVGGRARPHAWPFVSLQRLGCGHCGATLIAPNFVMSAAHCVANVNVRAVRVVLGAHNL 60
Db 34 IIGHEVTPHSRPMASVREGGQHCGFLRLARWVVSAAHCFSHRDLRTGLVVLGAHVL 93
Qy 61 SREPTQVFAVQRIEEN-CTDPVNLNDIVILQNGSATINANVOVAQLPAQGRRL--- 116
Db 94 STAEPTQVFGIDALTTHPDYHPMTHANDICLLRLNGSAVLGPAVGLLRPL--GRRARPP 151
Qy 117 GNGVQCLAMGWLGRNRGIASVLQELNVTV-----VTSLCRRSNVCTLV 161
Db 152 TAGTRCRVAGWGFVSDPEELPPGLMEAKVRVLDPDVCNSSWGHLTLTLMCTRSRSG----- 206
Qy 162 RGRQAGVCFGDSGLVNCGLIHGIASFVRGGCASGLYPDAPAPVAQFVNWIDSIIQR 219
Db 207 DSHRRGFCSDSGPLVCRNRAHGLVSFSLWCWGDPKTPDVTYQVSAFVAWIWDVVRR 264

Search completed: April 18, 2005, 13:02:20
Job time : 136 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 18, 2005, 12:39:38 ; Search time 44 Seconds
(without alignments)
478.897 Million cell updates/sec

Title: US-10-733-288A-4
Perfect score: 1140
Sequence: 1 IVGRRARPHAWPFVMSLQL.....PDFAFPAQVFWIDSIQR 219

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*

1: Pirl:.*
2: Pirl:.*
3: Pirl:.*
4: Pirl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1133	99.4	267	1 ELRHUL	leukocyte elastase
2	868.5	76.2	265	2 I48679	neutrophil elastase
3	637.5	55.9	256	1 PRHU3	protease 3 (EC 3
4	480	42.1	251	1 TRHUZ	azurocidin precurs
5	438	37.5	219	1 TRPGNZ	azurocidin - pig
6	379	33.2	286	1 ELPG	pancreatic elastas
7	366	32.1	266	1 ELRT1	pancreatic elastas
8	364	31.9	258	4 S70439	pancreatic elastas
9	364	31.9	267	4 A56615	pancreatic elastas
10	344.5	30.2	261	2 A40162	probable pancreati
11	343.5	30.1	282	1 A31372	cathepsin G (EC 3
12	341	29.9	258	2 I56220	granzyme A (EC 3.4
13	340.5	29.9	256	2 S69370	trypsin 2 - rat
14	338.5	29.7	255	2 A27122	duodenase - bovine
15	338.5	29.7	263	1 I55608	cathepsin G (EC 3
16	337	29.6	244	2 A34910	complement factor
17	336.5	29.5	259	1 WMS28	complement factor
18	336.5	29.5	259	2 A2823	pancreatic elastas
19	335	29.4	246	1 DBHU	complement factor
20	332.5	29.2	269	2 B26823	pancreatic elastas
21	332.5	29.2	271	1 ELRT2	pancreatic elastas
22	331.5	29.1	257	2 B45061	granzyme A (EC 3.4
23	331.5	29.1	260	2 A45061	granzyme A (EC 3.4
24	328.5	28.8	249	2 A55634	granzyme M (EC 3.4
25	327.5	28.7	271	2 A25528	pancreatic elastas
26	326.5	28.6	265	2 T10495	chymotrypsin (EC 3
27	325	28.5	236	2 A28566	T-cell suppressor
28	325	28.5	244	2 A46721	chymase (EC 3.4.21
29	322.5	28.3	226	1 KCUF	bradykinin (EC 3.4

RESULT 1

ELRHUL

N;Alternate names: inflammatory serine proteinase; medullasin; neutrophil elastase

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1990 #sequence revision 30-Jun-1990 #text change 09-Jul-2004

C;Accession: A31976; S04954; S06241; A27064; S00631; A28370; A34570; A05293; A25907; S1

R;Takahashi, H.; Nukiwa, T.; Yoshimura, K.; Quick, C.D.; States, D.J.; Holmes, M.D.; Wh

J. Biol. Chem. 263, 14739-14747, 1988

A;Title: Structure of the human neutrophil elastase gene.

A;Reference number: A31976; MUID:89008342; PMID:2902087

A;Accession: A31976

A;Molecule type: DNA

A;Residues: 1-267 <TAK>

A;Cross-references: UNIPROT:P08246; GB:M20203; GB:J04032; NID:g189147; PIDN:AAA36359.1;

R;Farley, D.; Travis, J.; Salvesen, G.

Biol. Chem. Hoppe-Seyler 370, 737-744, 1989

A;Title: The human neutrophil elastase gene. Analysis of the nucleotide sequence reveal

A;Reference number: S04954; MUID:89374820; PMID:2775493

A;Accession: S04954

A;Status: not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-267 <FAR>

R;Nakamura, H.; Okano, K.; Aoki, Y.; Shimizu, H.; Naruto, M.

Nucleic Acids Res. 15, 9601-9602, 1987

A;Title: Nucleotide sequence of human bone marrow serine protease (medullasin) gene.

A;Reference number: S06241; MUID:88067782; PMID:3479752

A;Accession: S06241

A;Status: preliminary; translation not shown

A;Molecule type: DNA

A;Residues: 1-267 <NAK>

A;Cross-references: EMBL:Y00477; NID:g34529; PIDN:CAA68537.1; PID:g296665

R;Okano, K.; Aoki, Y.; Sakurai, T.; Kajitani, M.; Kanai, S.; Shimizu, T.; Shimizu, H.;

J. Biochem. 102, 13-16, 1987

A;Title: Molecular cloning of complementary DNA for human medullasin: an inflammatory s

A;Reference number: A27064; MUID:88032918; PMID:2822677

A;Accession: A27064

A;Molecule type: mRNA

A;Residues: 30-267 <OKA>

A;Cross-references: EMBL:X05875; NID:g34532; PIDN:CAA29300.1; PID:g1335212

R;Farley, D.; Salvesen, G.; Travis, J.

Biol. Chem. Hoppe-Seyler 369(Suppl.), 3-7, 1988

A;Title: Molecular cloning of human neutrophil elastase.

A;Reference number: S00631; MUID:89076526; PMID:2462434

A;Accession: S00631

A;Molecule type: mRNA

A;Residues: 123-267 <FA2>

A;Cross-references: GB:M27783; NID:g182055; PIDN:AAA35792.1; PID:g182056

A;Note: the authors translated the codon TTC for residue 218 as Pro

R;Takahashi, H.; Nukiwa, T.; Bassett, P.; Crystal, R.G.

J. Biol. Chem. 263, 2543-2547, 1988

THIS PAGE BLANK (USP10)

A;Title: Myelomonocytic cell lineage expression of the neutrophil elastase gene.
A;Reference number: A28370; MUID:88115408; PMID:3422232
A;Accession: A28370
A;Molecule type: mRNA
A;Residues: 75-267 <TA2>
A;Cross-references: GB:J03545; NID:9182050; PIDN:AAA52378.1; PID:g182051
R;Okano, K.; Aoki, Y.; Shimizu, H.; Naruto, M.
Biochem. Biophys. Res. Commun. 167, 1326-1332, 1990
A;Title: Functional expression of human leukocyte elastase (HLE)/medullasin in eukaryotic cells.
A;Reference number: A34570; MUID:90211319; PMID:3222278
A;Accession: A34570
A;Molecule type: mRNA
A;Residues: 1-267 <OK2>
A;Cross-references: GB:M34379; NID:9187116; PIDN:AAA36173.1; PID:g307123
R;Travis, J.; Giles, P.J.; Porcella, L.; Reilly, C.F.; Baugh, R.; Powers, J.
in Protein Degradation in Health and Disease, Ciba Foundation Symposium 75, 51-68, 1980
A;Reference number: A94428
A;Accession: A05293
A;Molecule type: protein
A;Residues: 30-66, 'G', 68-73, 'D', 75, 78-82, 'E', 84-89, 'T', 91-94, 'P', 97-100, 'L', 102-103 <TR>
A;Experimental source: neutrophil granulocytes
R;Sinha, S.; Watorek, W.; Karr, S.; Giles, J.; Bode, W.; Travis, J.
Proc. Natl. Acad. Sci. U.S.A. 84, 2228-2232, 1987
A;Title: Primary structure of human neutrophil elastase.
A;Reference number: A25907; MUID:87175647; PMID:3550808
A;Accession: A25907
A;Molecule type: protein
A;Residues: 30-247 <SIN>
A;Note: the sequence from Fig. 1 is inconsistent with that from Fig. 2 in having 107-Asp
R;Green, B.G.; Weston, H.; Ashe, B.M.; Doherty, J.; Finke, P.; Hagmann, W.; Lark, M.; M
Arch. Biochem. Biophys. 286, 284-292, 1991
A;Title: PMN elastases: a comparison of the specificity of human isozymes and the enzyme
A;Reference number: S14736; MUID:91378304; PMID:1897955
A;Accession: S14736
A;Molecule type: protein
A;Residues: 30-50 <GRE>
A;Comment: This is a lysosomal proteinase found in the azurophil granules of neutrophils
C;Comment: This elastase cleaves preferentially bonds after Ala and Val. It is believed
C;Genetics:
A;Gene: GDB:ELA2
A;Cross-references: GDB:118792; OMIM:130130
A;Map position: 19p13.3-19p13.3
A;Introns: 23/1; 75/2; 122/3; 199/3
C;Superfamily: trypsin; trypsin homology
C;Keywords: emphysema; glycoprotein; hydrolase; leukocyte; lysosome; rheumatoid arthritis
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-29/Domain: propeptide #status predicted <PRO>
F;30-247/Product: leukocyte elastase #status experimental <MAT>
F;30-242/Domain: trypsin homology <TRI>
F;248-267/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;55-71,151-208,181-187,198-223/Disulfide bonds: #status experimental
F;70,117,202/Active site: His, Asp, Ser #status predicted
F;88/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;124,173/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 99.4%; Score 1133; DB 1; Length 267;
Best Local Similarity 99.4%; Pred. No. 5.6e-97;
Matches 218; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 IVGGRARPHAWPFVMSLQLRGFGCGATLIAPNFVMSAAHCVANVAVRVVVLGAHNL 60
DB 30 IVGGRARPHAWPFVMSLQLRGFGCGATLIAPNFVMSAAHCVANVAVRVVVLGAHNL 89
QY 61 SRREPTQVFAVQRIPEFGTDPVNLNDIVILQNGSATINAVQVLAQRRLLNGV 120
DB 90 SRREPTQVFAVQRIPEFGTDPVNLNDIVILQNGSATINAVQVLAQRRLLNGV 149
QY 121 QCLAMGWLGRNRIASVQLQELNVTVTSLCRSSNVCTLVGRQAGVCFGDSGPLVCN 180
DB 150 QCLAMGWLGRNRIASVQLQELNVTVTSLCRSSNVCTLVGRQAGVCFGDSGPLVCN 209
QY 181 GLIHGIASFVRGCGSLGYPDAPFAPVQFVNWIDSIIOR 219

Db 210 GLIHGIASFVRGCGSLGYPDAPFAPVQFVNWIDSIIOR 248

RESULT 2

I48679
neutrophil elastase - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I48679
R;Nuchprayoon, I.; Meyers, S.; Scott, L.M.; Suzow, J.; Hiebert, S.; Friedman, A.D.
Mol. Cell. Biol. 14, 5558-5568, 1994
A;Title: PEBP2/CBF, the murine homolog of the human myeloid AML1 and PEBP2 beta/CBF bet
1a.
A;Reference number: I48679; MUID:94305676; PMID:8035830
A;Accession: I48679
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-265 <RES>
A;Cross-references: UNIPROT:Q61515; EMBL:U04962; NID:9452556; PIDN:AAB60670.1; PID:9452
C;Genetics:
A;Introns: 22/1; 74/2; 121/3; 199/3
C;Superfamily: trypsin; trypsin homology
F;29-242/Domain: trypsin homology <TRY>

Query Match 76.2%; Score 868.5; DB 2; Length 265;
Best Local Similarity 75.9%; Pred. No. 1.4e-72;
Matches 167; Conservative 19; Mismatches 33; Indels 1; Gaps 1;

QY 1 IVGGRARPHAWPFVMSLQLRGFGCGATLIAPNFVMSAAHCVANVAVRVVVLGAHNL 60
DB 29 IVGGRARPHAWPFVMSLQLRGFGCGATLIAPNFVMSAAHCVANVAVRVVVLGAHNL 88
QY 61 SRREPTQVFAVQRIPEFGTDPVNLNDIVILQNGSATINAVQVLAQRRLLNGV 120
DB 89 SRREPTQVFAVQRIPEFGTDPVNLNDIVILQNGSATINAVQVLAQRRLLNGV 148
QY 121 QCLAMGWLGRNRIASVQLQELNVTVTSLCRSSNVCTLVGRQAGVCFGDSGPLVC 179
DB 149 QCLAMGWLGRNRIASVQLQELNVTVTSLCRSSNVCTLVGRQAGVCFGDSGPLVC 208
QY 180 NGLIHGIASFVRGCGSLGYPDAPFAPVQFVNWIDSIIOR 219
DB 209 NNLVQIGDSFIRGCGSLGYPDAPFAPVGEFVDWINSIIR 248

RESULT 3
PRH03
proteinase 3 (EC 3.4.21.-) precursor [validated] - human
N;Alternate names: AGP7; C-ANCA antigen; neutrophil proteinase 4; p29; Wegener's granul
N;Contains: myeloblastin
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
C;Accession: A45080; A43983; JH0331; A33751; S11091; A61176; A60148; A43982; A4;
R;Sturrock, A.B.; Franklin, K.F.; Rao, G.; Marshall, B.C.; Rebentisch, M.B.; Lemons, R.;
J. Biol. Chem. 267, 21193-21199, 1992
A;Title: Structure, chromosomal assignment, and expression of the gene for proteinase-3
A;Reference number: A45080; MUID:93016043; PMID:1400430
A;Accession: A45080
A;Molecule type: DNA
A;Residues: 1-254, 'P', <STU>
A;Cross-references: UNIPROT:P24158; GB:M97911
A;Note: sequence extracted from NCBI backbone (NCBIP:116205)
R;Zimmer, M.; Medcalf, R.L.; Fink, T.M.; Mattmann, C.; Lichter, P.; Jenne, D.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 8215-8219, 1992
A;Title: Three human elastase-like genes coordinately expressed in the myelomonocyte 11;
A;Reference number: A46268; MUID:92390417; PMID:1518849
A;Accession: A46268
A;Molecule type: DNA
A;Residues: 1-118, 'V', 120-134, 'AT', 137-256 <ZTM>
A;Note: sequence extracted from NCBI backbone (NCBIN:112898, NCBIN:112900, NCBIN:112902,
R;Labbaye, C.; Musette, P.; Cayre, Y.E.
Proc. Natl. Acad. Sci. U.S.A. 88, 9253-9256, 1991
A;Title: Wegener autoantigen and myeloblastin are encoded by a single mRNA.

THIS PAGE BLANK (USP 10)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 18, 2005, 12:40:23 ; Search time 43 Seconds
(without alignments)
380.189 Million cell updates/sec

Title: US-10-733-288A-4

Perfect score: 1140

Sequence: 1 IVGGRRARPHAWFMVSLQ.....PDFAFPAQFVNWIDSIQR 219

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000 ,

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/prodata/1/iaa/5A COMB.pap.*
2: /cgn2_6/prodata/1/iaa/5B COMB.pap.*
3: /cgn2_6/prodata/1/iaa/6A COMB.pap.*
4: /cgn2_6/prodata/1/iaa/6B COMB.pap.*
5: /cgn2_6/prodata/1/iaa/PCTUS COMB.pap.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1133	99.4	238	3	US-08-944-483-31
2	1133	99.4	238	6	Sequence 31, Appl
3	1133	99.4	238	6	Patent No. 5180819
4	1133	99.4	267	2	Sequence 46, Appl
5	791	69.4	271	3	Sequence 6, Appl
6	639.5	56.1	229	4	Sequence 27, Appl
7	639.5	56.1	231	4	Sequence 25, Appl
8	639.5	56.1	256	4	Sequence 23, Appl
9	639.5	56.1	256	4	Sequence 23, Appl
10	638.5	56.0	229	2	Sequence 20, Appl
11	638.5	56.0	229	4	Sequence 20, Appl
12	638.5	56.0	229	4	Sequence 20, Appl
13	638.5	56.0	229	5	Sequence 20, Appl
14	638.5	56.0	256	2	Sequence 4, Appl
15	632.5	55.5	229	3	Sequence 4, Appl
16	632.5	55.5	256	4	Sequence 30, Appl
17	581	51.0	214	6	Sequence 6271, Ap
18	581	51.0	214	6	Patent No. 5180819
19	572.5	50.2	215	6	Patent No. 5180819
20	572.5	50.2	215	6	Patent No. 5180819
21	485	42.5	222	2	Sequence 18, Appl
22	480	42.1	222	1	Sequence 9, Appl
23	480	42.1	222	1	Sequence 9, Appl
24	480	42.1	225	3	Sequence 32, Appl
25	480	42.1	251	4	Sequence 6112, Ap
26	480	42.1	255	4	Sequence 9690, Ap
27	477	41.8	221	2	Sequence 1, Appl

28 424 37.2 219 2 US-08-925-708-2 Sequence 2, Appl
29 377 33.1 240 1 US-08-278-091-11 Sequence 11, Appl
30 377 33.1 240 1 US-08-483-859-11 Sequence 11, Appl
31 377 33.1 240 1 US-08-472-173-11 Sequence 11, Appl
32 377 33.1 240 2 US-08-487-167-11 Sequence 11, Appl
33 377 33.1 240 2 US-08-482-816-11 Sequence 11, Appl
34 377 33.1 240 2 US-08-296-149-11 Sequence 11, Appl
35 377 33.1 240 2 US-08-801-499-11 Sequence 11, Appl
36 377 33.1 240 2 US-08-615-271-11 Sequence 11, Appl
37 377 33.1 240 3 US-09-074-660-11 Sequence 11, Appl
38 377 33.1 240 3 US-09-074-659-11 Sequence 11, Appl
39 377 33.1 240 3 US-09-106-468-11 Sequence 11, Appl
40 377 33.1 240 3 US-09-106-467-11 Sequence 11, Appl
41 377 33.1 240 3 US-09-106-467-11 Sequence 11, Appl
42 372 32.6 283 4 US-09-244-111-2 Sequence 2, Appl
43 364 31.9 133 4 US-09-949-016-7471 Sequence 7471, Ap
44 343.5 30.1 234 3 US-08-944-483-46 Sequence 46, Appl
45 343.5 30.1 268 4 US-09-949-016-10712 Sequence 10712, A

ALIGNMENTS

RESULT 1

US-08-944-483-31

; Sequence 31, Application US/08944483

; Patent No. 6232456

; GENERAL INFORMATION:

APPLICANT: COHEN, MAURICE

APPLICANT: COLPITTS, TRACEY L.

APPLICANT: FRIEDMAN, PAULA N.

APPLICANT: GRANADOS, EDWARD N.

APPLICANT: KLASS, MICHAEL R.

APPLICANT: RUSSELL, JOHN C.

APPLICANT: STEWART, KENT D.

APPLICANT: STROUPE, STEVEN D.

TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS

TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES

NUMBER OF SEQUENCES: 76

CORRESPONDENCE ADDRESS:

ADDRESSEE: Abbott Laboratories

STREET: 100 Abbott Park Road

CITY: Abbott Park

STATE: IL

COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/944,483

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Becker, Cheryl L.

REGISTRATION NUMBER: 35,441

REFERENCE/DOCKET NUMBER: 6183.US.01

TELECOMMUNICATION INFORMATION:

TELEPHONE: 847/935-1729

TELEFAX: 847/938-2623

TELEX:

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:

LENGTH: 238 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

Query Match 99.4%; Score 1133; DB 6; Length 238;
Best Local Similarity 99.5%; Pred. No. 2.9e-118;
Matches 218; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 IVGRRARPHAWPFMVSLQLRGHHFCGATLIAPNFVMSAAHCVANVNVRAVRVVLGAHNL 60
DB 1 IVGRRARPHAWPFMVSLQLRGHHFCGATLIAPNFVMSAAHCVANVNVRAVRVVLGAHNL 60

QY 61 SRREPTQVFAVORIFENGTDVNLNDIVILQNGSATINANVQVQLPAQGRRLGNGV 120
DB 61 SRREPTQVFAVORIFENGTDVNLNDIVILQNGSATINANVQVQLPAQGRRLGNGV 120

QY 121 QCLAMGWLGRNRGIASVLQELNVTVTSLCRSSNVCTLVGRQAGVCFDGSPLVCN 180
DB 121 QCLAMGWLGRNRGIASVLQELNVTVTSLCRSSNVCTLVGRQAGVCFDGSPLVCN 180

QY 181 GLIHGIASFVRGGCAGSLYDPAFAPVAFVFNWIDSIIQR 219
DB 181 GLIHGIASFVRGGCAGSLYDPAFAPVAFVFNWIDSIIQR 219

RESULT 4
US-08-978-404B-46
; Sequence 46, Application US/08978404B
; Patent No. 5968782
; GENERAL INFORMATION:
; APPLICANT: Stevens, Richard L.
; TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
; TITLE OF INVENTION: FIBRINOGEN
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02210-2211
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fast-SEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,404B
; FILING DATE: 25-NOV-97
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/032,354
; FILING DATE: 04-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Plumer, Elizabeth R.
; REGISTRATION NUMBER: 36,637
; REFERENCE/DOCKET NUMBER: B0801/7090
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; TELEX:
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5968782e
US-08-978-404B-46

Query Match 99.4%; Score 1133; DB 2; Length 267;
Best Local Similarity 99.5%; Pred. No. 3.4e-118;
Matches 218; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 IVGRRARPHAWPFMVSLQLRGHHFCGATLIAPNFVMSAAHCVANVNVRAVRVVLGAHNL 60
DB 30 IVGRRARPHAWPFMVSLQLRGHHFCGATLIAPNFVMSAAHCVANVNVRAVRVVLGAHNL 89

US-08-944-483-31
MOLECULE TYPE: No. 6232456e

Query Match 99.4%; Score 1133; DB 3; Length 238;
Best Local Similarity 99.5%; Pred. No. 2.9e-118;
Matches 218; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 IVGRRARPHAWPFMVSLQLRGHHFCGATLIAPNFVMSAAHCVANVNVRAVRVVLGAHNL 60
DB 1 IVGRRARPHAWPFMVSLQLRGHHFCGATLIAPNFVMSAAHCVANVNVRAVRVVLGAHNL 60

QY 61 SRREPTQVFAVORIFENGTDVNLNDIVILQNGSATINANVQVQLPAQGRRLGNGV 120
DB 61 SRREPTQVFAVORIFENGTDVNLNDIVILQNGSATINANVQVQLPAQGRRLGNGV 120

QY 121 QCLAMGWLGRNRGIASVLQELNVTVTSLCRSSNVCTLVGRQAGVCFDGSPLVCN 180
DB 121 QCLAMGWLGRNRGIASVLQELNVTVTSLCRSSNVCTLVGRQAGVCFDGSPLVCN 180

QY 181 GLIHGIASFVRGGCAGSLYDPAFAPVAFVFNWIDSIIQR 219
DB 181 GLIHGIASFVRGGCAGSLYDPAFAPVAFVFNWIDSIIQR 219

RESULT 2
5180819-4
; Patent No. 5180819
; APPLICANT: CAYRE, YVON
; TITLE OF INVENTION: PURIFIED MYELOBLASTIN, NUCLEIC ACID
; MOLECULE ENCODING SAME, AND USES THEREOF
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/455,614
; FILING DATE: 22-DEC-1989
; SEQ ID NO: 4:
; LENGTH: 238
5180819-4

Query Match 99.4%; Score 1133; DB 6; Length 238;
Best Local Similarity 99.5%; Pred. No. 2.9e-118;
Matches 218; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 IVGRRARPHAWPFMVSLQLRGHHFCGATLIAPNFVMSAAHCVANVNVRAVRVVLGAHNL 60
DB 1 IVGRRARPHAWPFMVSLQLRGHHFCGATLIAPNFVMSAAHCVANVNVRAVRVVLGAHNL 60

QY 61 SRREPTQVFAVORIFENGTDVNLNDIVILQNGSATINANVQVQLPAQGRRLGNGV 120
DB 61 SRREPTQVFAVORIFENGTDVNLNDIVILQNGSATINANVQVQLPAQGRRLGNGV 120

QY 121 QCLAMGWLGRNRGIASVLQELNVTVTSLCRSSNVCTLVGRQAGVCFDGSPLVCN 180
DB 121 QCLAMGWLGRNRGIASVLQELNVTVTSLCRSSNVCTLVGRQAGVCFDGSPLVCN 180

QY 181 GLIHGIASFVRGGCAGSLYDPAFAPVAFVFNWIDSIIQR 219
DB 181 GLIHGIASFVRGGCAGSLYDPAFAPVAFVFNWIDSIIQR 219

RESULT 3
5180819-4
; Patent No. 5180819
; APPLICANT: CAYRE, YVON
; TITLE OF INVENTION: PURIFIED MYELOBLASTIN, NUCLEIC ACID
; MOLECULE ENCODING SAME, AND USES THEREOF
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/455,614
; FILING DATE: 22-DEC-1989
; SEQ ID NO: 4:
; LENGTH: 238
5180819-4

```

:      Perez, Carl
:
: TITLE OF INVENTION: Compositions for the Inhibition of
:                      Protein Hormone Formation and Uses Thereof
:
:
: NUMBER OF SEQUENCES: 30
:
: CORRESPONDENCE ADDRESS:
:   ADDRESSEE: McAndrews, Held & Malloy
:   STREET: 500 West Madison - 34th Floor
:   CITY: Chicago
:   STATE: Illinois
:   COUNTRY: United States of America
:   ZIP: 60661
:
: COMPUTER READABLE FORM:
:

```

```

COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/395,456C
  FILING DATE: 28-Feb-1995
  CLASSIFICATION: <Unknown>
  ATTORNEY/AGENT INFORMATION:
    NAME: Pochopien, Donald J.
    REGISTRATION NUMBER: 32,167
    REFERENCE/DOCKET NUMBER: 0820.006/1296 11850US06
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 312/775-8000
    TELEFAX: 312/775-8100
    TELEX: <Unknown>
  INFORMATION FOR SEQ ID NO: 27:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 229 amino acids
      TYPE: amino acid
      TOPOLOGY: linear
    MOLECULE TYPE: protein
    SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-08-395-456C-27

```

Best Local Similarity 54.5%; Pred. NO. 3.4e-63;
Matches 121; Conservative 40; Mismatches 58; Indels 3; Gaps 1

QY	1	IVGRRRAPHAWPFMVSLQLR--GGHFCGATLIAPNFVMSAAHCVANVNVRAVRV	
Db	1	IVGHEAPQPHSRPYMASLQMRGNPQSHFCGGLIHPFVLTAAHCURDIPQLRLNVVV	
QY	58	HNLSRRREPTRQVFAVQRIEFENGTDVPVNLNDIVILQLNGSATINANVQVLAQLPAQGR	
Db	61	HNVRTQETPQQHFSVAQVFLNNDYDAENKLNLDILLQLSSPANLSASVATVQLPQQDQ	
QY	118	NGVQCLAMWGGLLGRNVRGIASVLQELNVTVTSLCRRSNVCTLVGRQAGVCFGDSG	
Db	121	HGTQCLAMWGVRGAHDPPAQVLQELNVTVTFFCRPHNICITFVPRRKAGICFGDSG	
QY	178	VGNGLIHGIASVFRGCCASGLYPDAPAPVAQFNVWIDSIIQR	219
Db	181	ICDGIITQIGDSFVWGCAATRLFPDFETRVALYVDWIRSLRR	222

RESULT 7
US-08-395-456C-25
; Sequence 25, Application US/08395456C
; Patent No. 6586222

AFFILIATION: HASENBECK, ROBERT E.
 JEWELL, DAVID A.
 KOTHS, KIRSTON E.
 KRIEGLER, MICHAEL
 PEREZ, CARL
 TITLE OF INVENTION: COMPOSITIONS FOR THE INHIBITION OF
 PROTEIN HORMONE FORMATION AND USES THEREOF
 NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MCANDREWS, HEID & MALLOY

```

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/395,456C
FILING DATE: 28-Feb-1995
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Pochopien, Donald J.
REGISTRATION NUMBER: 32,167
REFERENCE/DOCKET NUMBER: 0820.006/1296 1185OUS06
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/775-8000
TELEFAX: 312/775-8100
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 256 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-08-395-456C-23

Query Match          56.1%; Score 639.5; DB 4; Length 256;
Best Local Similarity 54.5%; Pred. No. 4e-63;
Matches 121; Conservative 40; Mismatches 58; Indels 3; Gaps 1

QY      1   IVGGRRARPHAWPMVSLQLR---GGHFCGATLIAPNFWSAAHCVANVVPAVRVLGA 57
         ||| :||: |:||: |::| |::| |::| |::| |:|: |::| |::| |::| |::|
DB       28   IVGCGHEAQHSRPYMASLQMGRNPGSHFGCTGLIHESFLVTAAACLRDIPQLRVNVILGA 87
         ||| :||: |:||: |::| |::| |::| |::| |:|: |::| |::| |::| |::|

QY      58   HNLSRRPTKQVFVAQRIFENGTDPVNLLNDIVILONGSATINNVOVALPQAQRRLIG 117
         ||| :||: |:||: |::| |::| |::| |::| |:~::~|: ~::~|: ~::~|: ~::~|:
DB       88   HNVRTQETQHFSVAOQPLNNVDANKLNLDILLIOLSSPANLSASVAVTQLPQQQPVP 147
         ||| :||: |:||: |::| |::| |::| |::| |:~::~|: ~::~|: ~::~|: ~::~|:

QY     118   NGVCALMGWELLGNRGIAVSLOELNNVTTVTSCLRNRNVCTLVRGRAGCVCFSGDSGPL 177
         ||| :||: |:||: |::| |::| |::| |::| |:~::~|: ~::~|: ~::~|: ~::~|:
DB     148   GTQCCLAMGWCRVGAHDPPAQLVELNNTVTTFRCRPNICTFPVPRRKAGICFGDSGGPL 207

QY     178   VCNGLIHGIASFVGGCASGLYPDADAFAPAQFNWNIDSIIR 219
         ||| :||: |:||: |::| |::| |::| |::| |:~::~|: ~::~|: ~::~|: ~::~|:
DB     208   ICDDGIQGIDSFIWGCAITLPDFDTFRVALYVDWINSTLRR 249

RESULT 9
US-08-487-453A-23
Sequence 23, Application US/08487453A
Patent No. 6599706
GENERAL INFORMATION:
APPLICANT: Halenbeck, Robert F.
APPLICANT: Jewell, David A.
APPLICANT: Koths, Kirston E.
APPLICANT: Kriegler, Michael
APPLICANT: Perez, Carl
TITLE OF INVENTION: Recombinant PR-3 and Assays Employing the Same
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESSES:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,453A
FILING DATE:
```

```

; TELEFAX: 312/707-9155
; TELEX:
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-394-600B-20

Query Match 56.0%; Score 638.5; DB 2; Length 229;
Best Local Similarity 54.1%; Pred. No. 4.4e-63;
Matches 120; Conservative 41; Mismatches 58; Indels 3; Gaps 1;

QY 1 IVGGREARPHAWPFMVSLOLR---GGHFCGATLIAPNFVMSAAHCYANVNVRAVRVVILGA 57
DB 1 IVGGHEAQPHSRPYMASLQWRGNPGSHFCGGTLIHPFVLTAACLRDIPQRLVNVVILGA 60
QY 58 HNLRSREPTQTVAVORIEFENGTDTPVNLNLDIVILQNGSATNNANVQVLAQLPAQGRRLG 117
DB 61 HNYRTQPTQQHFSAVQVFLNNYDAENKLNLDVLLIQLSSPANLSASVATVQLPQQDQVP 120
QY 118 NGVQCLAMGGLGRNGRTASVLQELNVTVTSLCRSSNVCTLVGRQAGVCFGDSGSL 177
DB 121 HGTQCLAMGNGRVGADHPAQVQLQELNVTVTFFCPHNICTVPRKKAGICFGDSGSL 180
QY 178 VCNGLIHGIASFVRGGCAGSLYDPAFAPVAQFVNWIDSIQR 219
DB 181 ICDGIIGQDSFVWGCATLFFDFPTRVALYVDWIRSLRR 222

RESULT 11
US-08-395-456C-20
; Sequence 20, Application US/08395456C
; Patent No. 6586222
; GENERAL INFORMATION:
; APPLICANT: Halenbeck, Robert F.
; Jewell, David A.
; Koths, Kirston E.
; Kriegler, Michael
; Perez, Carl
; TITLE OF INVENTION: Compositions for the Inhibition of
; Protein Hormone Formation and Uses Thereof
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy
; STREET: 500 West Madison - 34th Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/395,456C
; FILING DATE: 28-Feb-1995
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Pochopien, Donald J.
; REGISTRATION NUMBER: 32,167
; REFERENCE/DOCKET NUMBER: 0820.006/1296 11850US06
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/775-8000
; TELEFAX: 312/775-8100
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 18, 2005, 12:27:28 ; Search time 174 Seconds
(without alignments)
486.785 Million cell updates/sec

Title: US-10-733-288A-4
Perfect score: 1140
Sequence: 1 IVGGRRRPHAWPFVMSLQL.....PDAFAPVAQFVNWDISIIR 219

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 385760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Match	Length	DB ID	Description
1	1133	99.4	238	7 ADJ68391	Adj68391 Human hea
2	1133	99.4	247	4 AAB55525	AAB55525 Human ela
3	1133	99.4	267	1 AAP80335	AAP80335 Sequence
4	1133	99.4	267	2 AAW64262	AAW64262 Human neu
5	1133	99.4	267	8 ADK42607	ADK42607 Human neu
6	1123	98.5	218	7 ADJ68281	Adj68281 Human hea
7	1114	97.7	218	5 AAU75897	AAU75897 Human leu
8	1064	93.3	257	5 ABP69417	ABP69417 Human pol
9	875.5	76.8	265	2 AAW70534	AAW70534 Mouse ser
10	872.5	76.5	265	2 AAR08269	AAR08269 Mouse ser
11	639.5	56.1	256	2 AAR85639	AAR85639 MY17 prep
12	639.5	56.1	256	7 ABW02656	ABW02656 Human pre
13	638.5	56.0	229	7 ABW02654	ABW02654 Human mat
14	638.5	56.0	256	2 AAR45403	AAR45403 Deduced s
15	638.5	56.0	256	7 ABW02646	ABW02646 Human pre
16	637.5	55.9	229	8 ADM67204	ADM67204 Human hom
17	637.5	55.9	229	7 ABW02679	ABW02679 Human mat
18	635.5	55.7	229	7 ABW02678	ABW02678 Human mat
19	635.5	55.7	253	8 ADM67203	ADM67203 Murine ad
20	634.5	55.7	229	7 ABW02676	ABW02676 Human mat
21	633.5	55.6	229	7 ABW02677	ABW02677 Human mat
22	632.5	55.5	229	7 ABW02680	ABW02680 Human mat
23	632.5	55.5	237	2 AAR20509	AAR20509 Human pro
24	632.5	55.5	256	5 ABB6770	ABB6770 Human pro
25	632.5	55.5	256	8 ADQ14416	ADQ14416 Human mye

26	632.5	55.5	256	8 ADR41702	ADR41702 Wegener's
27	569.5	50.0	215	2 AAR13036	AAR13036 Myeloblas
28	485.5	42.6	255	8 ADI16330	ADI16330 Human pro
29	485	42.5	222	2 AAW73210	AAW73210 CAP37 pro
30	483	42.4	225	7 ADE11551	ADE11551 Human mat
31	481	42.2	225	3 AAY71881	AAY71881 Human hep
32	480	42.1	222	2 AAR41935	AAR41935 Recombina
33	480	42.1	222	7 ADG42088	ADG42088 Human pol
34	480	42.1	225	2 AAW88362	AAW88362 Human mat
35	480	42.1	225	2 AAY21551	AAY21551 Human hep
36	480	42.1	225	2 AAW88118	AAW88118 Mature hu
37	480	42.1	225	3 AAY71883	AAY71883 Human hep
38	480	42.1	225	3 AAY71876	AAY71876 Human mat
39	480	42.1	225	4 AAY71891	AAY71891 Human mat
40	480	42.1	225	7 ADE11587	ADE11587 Human hep
41	480	42.1	225	8 ADK42019	ADK42019 Human hep
42	480	42.1	232	2 AAW88364	AAW88364 Human pro
43	480	42.1	232	2 AAY21550	AAY21550 Human hep
44	480	42.1	232	2 AAW88120	AAW88120 Human hep
45	480	42.1	232	3 AAY71877	AAY71877 Human pre

ALIGNMENTS

RESULT 1
ADJ68391

ID ADJ68391 standard; protein; 238 AA.

XX ADJ68391;

DT 06-MAY-2004 (first entry)

DE Human heat mitochondrial protein as a therapeutic target SegID197.

KW mitochondrial; human; screening assay; diabetes mellitus;

KW Huntington's disease; osteoarthritis;

KW Leber's hereditary optic neuropathy; LHON;

KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;

KW myoclonic epilepsy tagged red fibre syndrome; MERRF; cancer;

KW neuroprotective; nontropic; antidiabetic; anticonvulsant; antiarthritic;

KW osteopathic; ophthalmological; cytostatic.

OS Homo sapiens.

XX XX

PN WO2003087768-A2.

XX XX

PD 23-OCT-2003.

XX XX

PF 04-APR-2003; 2003WO-US010870.

XX XX

PR 12-APR-2002; 2002US-0372843P.

PR 17-JUN-2002; 2002US-0389987P.

PR 20-SEP-2002; 2002US-0412418P.

XX XX

PA (MITO-) MITOKOR.

PA (BUCK-) BUCK INST AGE RES.

XX XX

PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;

PI Warnock DE;

XX XX

DR WPI; 2003-845369/78.

XX XX

PT Identifying a mitochondrial target for drug screening assays and for

PT treating diseases associated with altered mitochondrial function,

PT comprises detecting a modified polypeptide in a sample and correlating

PT with the disease.

XX XX

PS Claim 1; SEQ ID NO 197; 180pp; English.

XX XX

CC This invention relates to novel mitochondrial targets that can be used

CC for therapeutic intervention in treating a disease associated with

CC altered mitochondrial function. Specifically, it refers to a method for

CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, neurotropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cytotstatic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.

XX Sequence 238 AA;
SQ
Query Match 99.4%; Score 1133; DB 7; Length 238;
Best Local Similarity 99.5%; Pred. No. 4.6e-68;
Matches 218; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 IVGGRRARPHAPFVMSVLSQLRGGHFCGATLIAPNFVMSAAHCVANVRAVRVVLGAHNL 60
DB 1 IVGGRRARPHAPFVMSVLSQLRGGHFCGATLIAPNFVMSAAHCVANVRAVRVVLGAHNL 60
QY 61 SRREPTQVFAVQRIFFENGTDVFNLLNDIVILQNGSATINANVOVAQLPAQGRRLGNGV 120
DB 61 SRREPTQVFAVQRIFFENGTDVFNLLNDIVILQNGSATINANVOVAQLPAQGRRLGNGV 120
QY 121 QCLAMGWLLGRNRGSIASVQLQELNVTVVTSLCRRSNVCTLVGRQAGVCFDGSGLVNCN 180
DB 121 QCLAMGWLLGRNRGSIASVQLQELNVTVVTSLCRRSNVCTLVGRQAGVCFDGSGLVNCN 180
QY 181 GLIHGIASFVRGGCAGSLYDPDAFAPVAQFVNWIDSIIQR 219
DB 181 GLIHGIASFVRGGCAGSLYDPDAFAPVAQFVNWIDSIIQR 219

RESULT 2
AAB55525
ID AAB55525 standard; protein; 247 AA.
XX
AC AAB55525;
DT 07-MAR-2001 (first entry)
DE Human elastase variant protein SEQ ID NO:95.
KW Human; elastase; variant; substrate; mutant; mutagenesis; histidine;
KW human neutrophil elastase; H43A; cytotstatic; proteolysis; ADEPT;
KW antibody-directed enzyme activated prodrug therapy.
OS Homo sapiens.
XX
FN WO200068363-A2.
XX 16-NOV-2000.
XX
PF 04-MAY-2000; 2000WO-US006692.
XX
PR 05-MAY-1999; 99US-0132640P.
XX
PA (GETH) GENENTECH INC.
XX
PI Carter PJ, Dall'acqua W, Rodrigues M;
XX
XX WPI; 2001-007389/01.
DR N-PSDB; AAC88022.
XX
PT Elastase variant (H43A) having altered substrate specificity useful for
PT antibody-directed enzyme activated prodrug therapy.
XX
XX Disclosure; Fig 2; 79pp; English.
PS
XX The present invention describes a purified elastase variant (I) with an

CC amino acid sequence different from that of a precursor elastase, the
CC difference comprising a substitution of an active site histidine residue
CC corresponding to residue 43 in human neutrophil elastase with a different
CC amino acid residue so that (i) has substrate specificity substantially
CC different from the precursor elastase. (i) has cytotstatic activity, and
CC can be used in antibody-directed enzyme activated prodrug therapy. The
CC elastase variant can be used to cleave a particular substrate, especially
CC those containing histidine residues at the substrate site. Site-specific
CC proteolysis is useful in therapeutic applications, e.g. for antibody-
CC directed enzyme activated prodrug therapy (ADEPT), AAC88022, AAC88023 and
CC AAB55432 to AAB55526 represent sequences used in the exemplification of
CC the present invention

XX Sequence 247 AA;
SQ
Query Match 99.4%; Score 1133; DB 4; Length 247;
Best Local Similarity 99.5%; Pred. No. 4.8e-68;
Matches 218; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 IVGGRRARPHAPFVMSVLSQLRGGHFCGATLIAPNFVMSAAHCVANVRAVRVVLGAHNL 60
DB 5 IVGGRRARPHAPFVMSVLSQLRGGHFCGATLIAPNFVMSAAHCVANVRAVRVVLGAHNL 64
QY 61 SRREPTQVFAVQRIFFENGTDVFNLLNDIVILQNGSATINANVOVAQLPAQGRRLGNGV 120
DB 65 SRREPTQVFAVQRIFFENGTDVFNLLNDIVILQNGSATINANVOVAQLPAQGRRLGNGV 124
QY 121 QCLAMGWLLGRNRGSIASVQLQELNVTVVTSLCRRSNVCTLVGRQAGVCFDGSGLVNCN 180
DB 125 QCLAMGWLLGRNRGSIASVQLQELNVTVVTSLCRRSNVCTLVGRQAGVCFDGSGLVNCN 184
QY 181 GLIHGIASFVRGGCAGSLYDPDAFAPVAQFVNWIDSIIQR 219
DB 185 GLIHGIASFVRGGCAGSLYDPDAFAPVAQFVNWIDSIIQR 223

RESULT 3
AAP80335
ID AAP80335 standard; protein; 267 AA.
XX
AC AAP80335;
DT 25-MAR-2003 (revised)
DT 04-OCT-1990 (first entry)
DE Sequence of serine protease (SP) of human myeloid cell origin and leader
DE peptide.
KW Serine protease; myeloid cell; intravascular coagulation treatment;
KW enzyme.
OS Homo sapiens.
XX
FN Key Location/Qualifiers
FT Peptide 1..29
FT Protein 30..267
XX
PN WO8806621-A.
XX
XX 07-SEP-1988.
XX
PF 26-FEB-1988; 88WO-JP000205.
XX
PR 05-MAR-1987; 87JP-00050676.
PR 09-SEP-1987; 87JP-00225540.
XX
PA (TORA) TORAY IND INC.
PA (AOKI/) AOKI Y.
XX
PI Aoki Y, Okano K, Naruto M, Shimizu H, Nakamura H;
XX
XX WPI; 1988-271161/38.
DR N-PSDB; AAN80315.

XX Serine protease of human myeloid cell origin - useful in disseminated
PT intravascular coagulation treatment.
XX
XX Disclosure; Fig 6; 52pp; Japanese.
XX
XX A SP of human myeloid cell origin is new. Also new are precursors of SP
CC having an N-terminal splittable or signal peptide; DNA sequences coding
CC for SP and precursors and transcription-controlling DNA sequence required
CC for expression of the gene. SP has antithrombotic activity, useful in
CC disseminated intravascular coagulation. By expression of protease gene in
CC suitable transformed organism SP can be obtained in large quantity. SP
CC DNA selected and cloned from a library of human myeloid cell origin,
CC inserted in suitable vector and expressed in transformant by a suitable
CC organism such as E.coli HMS-174 or HB-101 a yeast. (Updated on 25-MAR-
CC 2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 267 AA;

Query Match 99.4%; Score 1133; DB 1; Length 267;
Best Local Similarity 99.5%; Pred. No. 5.1e-68;
Matches 218; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 IVGRRARPHAPFPMVSLQRLGCGHFCGATLIAPNFVMSAAHCYANVNVRAVRVVLGAHNL 60
DB 30 IVGRRARPHAPFPMVSLQRLGCGHFCGATLIAPNFVMSAAHCYANVNVRAVRVVLGAHNL 89
QY 61 SRREPTQVFAVQRIPEFGTDPVNLNDIVILQNGSATINANVQVAPQAGRRILNGV 120
DB 90 SRREPTQVFAVQRIPEFGTDPVNLNDIVILQNGSATINANVQVAPQAGRRILNGV 149
QY 121 QCLAMGWLGRNRIASVQLQELNVTVTSLCRSSNVCTLVGRQAGVCFGDSGPLVCN 180
DB 150 QCLAMGWLGRNRIASVQLQELNVTVTSLCRSSNVCTLVGRQAGVCFGDSGPLVCN 209
QY 181 GLIHGTASFVRGCGASGLYPDAPAPVAFVFNWIDSIIQR 219
DB 210 GLIHGTASFVRGCGASGLYPDAPAPVAFVFNWIDSIIQR 248

RESULT 4
AAW64262
ID AAW64262 standard; protein; 267 AA.
XX
XX AAW64262;
AC
XX
XX 24-NOV-1998 (first entry)
DT
XX
XX Human neutrophil elastase.
DE
XX MCP-7; mast cell protease 7; tryptase-7; serine protease; human;
KW elastase; blood clot; anticoagulant; myocardial infarction; reocclusion;
KW thromboembolism; cerebral embolism; thrombosis; therapy.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Binding-site 55..68
FT /note= "putative substrate binding site"
FT
XX
XX WO9824886-A1.
PN
XX
XX 11-JUN-1998.
PD
XX
XX 25-NOV-1997; 97WO-US021620.
XX
XX 04-DEC-1996; 96US-0032354P.
XX
XX (BGHM) BRIGHAM & WOMENS HOSPITAL.
PA
XX Stevens RL;
PI
XX WPI; 1998-333308/29.
DR

XX New compositions containing tryptase-7, e.g. mouse mast cell protease-7 -
PT are used to treat clot formation in e.g. myocardial infarction,
XX reocclusion following angioplasty or pulmonary thrombo-embolism.
XX
XX Example; Page 78-79; 92pp; English.
XX
XX This polypeptide comprises the loop regions in the vicinity of the
CC putative substrate binding site of human neutrophil elastase. The
CC crystallographic structure of this region was used as a template
CC structure to model the structure of the substrate-binding pocket of mouse
CC mast cell protease 7 (MCP-7, see AAM64233). The invention relates to
CC MCP-7 and related tryptase-7 proteases that can be used to prevent or
CC inhibit fibrin clot formation. Such proteases can be used to treat
CC disorders mediated by undesirable thrombus clot formation such as
CC myocardial infarction and reocclusion following angioplasty of blood
CC clots associated with pulmonary thromboembolism, deep vein thrombosis,
CC cerebral embolism, renal vein and peripheral arterial thrombosis
XX
SQ Sequence 267 AA;

Query Match 99.4%; Score 1133; DB 2; Length 267;
Best Local Similarity 99.5%; Pred. No. 5.1e-68;
Matches 218; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 IVGRRARPHAPFPMVSLQRLGCGHFCGATLIAPNFVMSAAHCYANVNVRAVRVVLGAHNL 60
DB 30 IVGRRARPHAPFPMVSLQRLGCGHFCGATLIAPNFVMSAAHCYANVNVRAVRVVLGAHNL 89
QY 61 SRREPTQVFAVQRIPEFGTDPVNLNDIVILQNGSATINANVQVAPQAGRRILNGV 120
DB 90 SRREPTQVFAVQRIPEFGTDPVNLNDIVILQNGSATINANVQVAPQAGRRILNGV 149
QY 121 QCLAMGWLGRNRIASVQLQELNVTVTSLCRSSNVCTLVGRQAGVCFGDSGPLVCN 180
DB 150 QCLAMGWLGRNRIASVQLQELNVTVTSLCRSSNVCTLVGRQAGVCFGDSGPLVCN 209
QY 181 GLIHGTASFVRGCGASGLYPDAPAPVAFVFNWIDSIIQR 219
DB 210 GLIHGTASFVRGCGASGLYPDAPAPVAFVFNWIDSIIQR 248

RESULT 5
ADK42607
ID ADK42607 standard; protein; 267 AA.
XX
XX ADK42607;
AC
XX
XX 20-MAY-2004 (first entry)
DT
XX
XX Human neutrophil elastase.
DE
XX Human; heparin binding protein; HBP; neutrophil elastase; antibacterial;
KW cytokine IL-6; monocyte; bacterial infection; sepsis; septic shock;
KW disseminated intravascular coagulation; meningococcal meningitis;
KW pneumococcal pneumonia; inflammatory response; cell apoptosis;
KW suppressed immune system; cancer; autoimmune diseases; trauma.
XX
XX Homo sapiens.
OS
XX
XX WO2004016653-A2.
PN
XX
XX 26-FEB-2004.
PD
XX
XX 14-AUG-2003; 2003WO-DK000542.
XX
XX 15-AUG-2002; 2002DK-00001212.
PR
XX 19-AUG-2002; 2002US-0404155P.
PR
XX 27-JUN-2003; 2003DK-00000987.
XX
XX (LEUK-) LEUKETOCH AS.
PA
XX Djurup R, Flodgaard HJ, Norris K;
PI

XX WPI; 2004-257185/24.
DR N-PSDB; ADK42607.
XX
XX New peptides of heparin-binding protein and/or human neutrophil elastase
PT for manufacturing a medicament for the treatment of e.g. bacterial
PT infections, disseminated intravascular coagulation, cancer or autoimmune
PT diseases.
XX
XX Claim 52; SEQ ID NO 589; 211pp; English.
XX
XX The invention relates to an antibacterial peptide conforming to the
CC generic peptide sequence appearing as ADK42632, the motif being derived
CC from analysis of the protein sequences of human heparin binding protein,
CC hBHP, pig pHP and human neutrophil elastase (hNLE). Also included are a
CC process for producing the new peptide (comprising providing an expression
CC vector containing a DNA sequence encoding one or more of the above-
CC mentioned amino acid sequences, transforming host cells with the vector,
CC culturing the transformed host cells and purifying the expressed peptide)
CC and a pharmaceutical composition comprising the new peptide. The peptide
CC is capable of inhibiting or stimulating the secretion of cytokine IL-6
CC from monocytes. The peptides are useful in manufacturing a medicament for
CC the treatment of Gram-negative or Gram-positive bacterial infection, such
CC as sepsis, severe sepsis, septic shock, disseminated intravascular
CC coagulation, meningococcal meningitis or pneumococcal pneumonia. These
CC may also be used in manufacturing a medicament for the stimulation or
CC inhibition of inflammatory response, for the prevention of cell
CC apoptosis, or for the treatment of individuals having suppressed immune
CC system, cancer, autoimmune diseases and/or trauma. The present sequence
CC represents human neutrophil elastase.
XX
XX Sequence 267 AA;
SQ
Query Match 99.4%; Score 1133; DB 8; Length 267;
Best Local Similarity 99.5%; Pred. No. 5.1e-68;
Matches 218; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 IVGRRARPHAPFWVSLQLRGHCATLIAPNFVMSAAHCVANVAVRVVLGAHNL 60
DB 30 IVGRRARPHAPFWVSLQLRGHCATLIAPNFVMSAAHCVANVAVRVVLGAHNL 89
QY 61 SRREPTQVFAVQRIFFENGTDVFNLLNDIVILQNGSATINANVQVLAQRRLLNGV 120
DB 90 SRREPTQVFAVQRIFFENGTDVFNLLNDIVILQNGSATINANVQVLAQRRLLNGV 149
QY 121 QCLAMGWLLGNRGIAVQLQELNVVTSLCRRSNVCTLVGRQAGVCFGDSGPLVCN 180
DB 150 QCLAMGWLLGNRGIAVQLQELNVVTSLCRRSNVCTLVGRQAGVCFGDSGPLVCN 209
QY 181 GLIHGIASFVRGGCAGSLYPDAFAPVAFVQFVNWIDSIIQR 219
DB 210 GLIHGIASFVRGGCAGSLYPDAFAPVAFVQFVNWIDSIIQR 248
RESULT 6
ADJ68281
ID ADJ68281 standard; protein; 218 AA.
XX
AC ADJ68281;
XX
XX 06-MAY-2004 (first entry)
XX
XX Human heat mitochondrial protein as a therapeutic target SeqID87.
XX
XX mitochondrial; human; screening assay; diabetes mellitus;
KW Huntington's disease; osteoarthritis; LHON;
KW Leber's hereditary optic neuropathy; LHON;
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
KW osteopathic; ophthalmological; cytostatic.
XX
OS Homo sapiens.

XX WO2003087768-A2.
PN
XX
PD 23-OCT-2003.
XX
XX 04-APR-2003; 2003WO-US010870.
PF
XX
PR 12-APR-2002; 2002US-0372843P.
PR 17-JUN-2002; 2002US-038987P.
PR 20-SEP-2002; 2002US-0412418P.
XX
XX (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
XX
XX Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GW;
PI Warnock DE;
XX
XX WPI; 2003-845369/78.
DR
XX
XX Identifying a mitochondrial target for drug screening assays and for
PT treating diseases associated with altered mitochondrial function,
PT comprises detecting a modified polypeptide in a sample and correlating
PT with the disease.
XX
XX Claim 1; SEQ ID NO 87; 180pp; English.
PS
XX
XX This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, nootropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cytostatic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.
XX
XX Sequence 218 AA;
SQ
Query Match 98.5%; Score 1123; DB 7; Length 218;
Best Local Similarity 99.1%; Pred. No. 2e-67;
Matches 216; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 IVGRRARPHAPFWVSLQLRGHCATLIAPNFVMSAAHCVANVAVRVVLGAHNL 60
DB 1 IVGRRARPHAPFWVSLQLRGHCATLIAPNFVMSAAHCVANVAVRVVLGAHNL 60
QY 61 SRREPTQVFAVQRIFFENGTDVFNLLNDIVILQNGSATINANVQVLAQRRLLNGV 120
DB 61 SRREPTQVFAVQRIFFENGTDVFNLLNDIVILQNGSATINANVQVLAQRRLLNGV 120
QY 121 QCLAMGWLLGNRGIAVQLQELNVVTSLCRRSNVCTLVGRQAGVCFGDSGPLVCN 180
DB 121 QCLAMGWLLGNRGIAVQLQELNVVTSLCRRSNVCTLVGRQAGVCFGDSGPLVCN 180
QY 181 GLIHGIASFVRGGCAGSLYPDAFAPVAFVQFVNWIDSIIQ 218
DB 181 GLIHGIASFVRGGCAGSLYPDAFAPVAFVQFVNWIDSIIQ 218
RESULT 7
AAU75897
ID AAU75897 standard; peptide; 218 AA.
XX
AC AAU75897;
XX
XX 08-MAY-2002 (first entry)
XX

```
DE Human leukocyte elastase.
XX
KW Human; alpha1 protease inhibitor; factor IX activating protein;
KW anticoagulant; thrombolytic; thrombosis; leukocyte elastase;
KW blood coagulation.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 218
FT /label= Unknown
XX
XX
PN EP1174498-A2.
XX
XX 23-JAN-2002.
XX
XX 22-MAY-2001; 2001EP-00112430.
XX
XX 24-MAY-2000; 2000JP-00153096.
XX
XX (RIKE ) RIKEN KK.
XX
XX Kaibara M, Iwata H, Takio K, Dohmae N;
XX WPI; 2002-156689/21.
XX
XX Novel blood coagulation factor IX-activating protein useful for
XX diagnosing, treating and preventing diseases associated with abnormal
XX blood coagulation, is present in erythrocyte membrane and activates
XX Factor IX.
XX
XX Example 1; Fig 4; 29pp; English.
XX
XX The invention relates to a blood coagulation factor IX-activating protein
XX derived from a mammal and having a molecular weight of approximately
XX 29kDa as measured by sodium dodecyl sulphate-polyacrylamide gel
XX electrophoresis (SDS-PAGE). The factor is present in the erythrocyte
XX membrane, and acts on blood coagulation factor IX to activate it. The
XX activity of the factor is inhibited in the presence of an alpha1-protease
XX inhibitor or soybean trypsin inhibitor. Also included are an antibody
XX which recognises the factor and detecting a blood coagulation factor IX-
XX activating ability, by detecting or measuring the factor in a biological
XX sample. The factor and the antibody are useful for diagnosis, prevention
XX and/or treatment of diseases associated with blood coagulation, e.g.
XX thrombosis. The present sequence is the closest database match to the
XX partial sequence of the blood coagulation factor IX-activating protein
XX appearing as AAU75896, and is human leukocyte elastase
XX
XX Sequence 218 AA;
XX
XX Query Match 97.7%; Score 1114; DB 5; Length 218;
XX Best Local Similarity 99.1%; Pred. No. 7.9e-67;
XX Matches 215; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 IVGGRARPHAWPFMVSLQLRGCHFCGATLIAPNFVMSAAHCYANNVAVRVVLGAHNL 60
Db 1 IVGGRARPHAWPFMVSLQLRGCHFCGATLIAPNFVMSAAHCYANNVAVRVVLGAHNL 60
QY 61 SRREPTQVFAVQRIFFENGCTDPVNLNDIVILQLNGSATINANVQVQALPAQGRRLGNGV 120
Db 61 SRREPTQVFAVQRIFFENGCTDPVNLNDIVILQLNGSATINANVQVQALPAQGRRLGNGV 120
QY 121 QCLAMGWLGNRGVIAVQLNVTVTSLCRSSNVCTLVGRQAGVCGDGSPLVCN 180
Db 121 QCLAMGWLGNRGVIAVQLNVTVTSLCRSSNVCTLVGRQAGVCGDGSPLVCN 180
QY 181 GLIHGTASFVRGCGASGLYPDAFPAVQFVNWIDSII 217
Db 181 GLIHGTASFVRGCGASGLYPDAFPAVQFVNWIDSII 217
RESULT 8
ABP69417
```

```
ID ABP69417 standard; protein; 257 AA.
XX
AC ABP69417;
XX
DT 20-JAN-2003 (first entry)
XX
DE Human polypeptide SEQ ID NO 1464.
XX
XX Human; genome mapping; gene therapy; food supplement; virus; fungus;
XX cell-proliferative disorder; neurodegenerative disease; bacterial;
XX Parkinson's disease; Alzheimer's disease; autoimmune disease;
XX multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
XX arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;
XX antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
XX haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide;
XX antiarthritic.
XX
OS Homo sapiens.
XX
XX WO200270539-A2.
XX
XX 12-SEP-2002.
XX
XX 05-MAR-2002; 2002WO-US005095.
XX
XX 05-MAR-2001; 2001US-00799451.
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;
XX Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
XX Wehrman T, Wang J, Wang D, Drmanac RT;
XX
XX WPI; 2002-759812/82.
XX N-PSDB; ABZ11634.
XX
XX New polynucleotides comprising sequences assembled from expressed
XX sequence tags (ESTs), useful for treating cell-proliferative,
XX neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
XX or coagulation disorders.
XX
XX Claim 9; SEQ ID NO 1464; 1012pp + Sequence Listing; English.
XX
XX The invention relates to an isolated polynucleotide (I) comprising a
XX nucleotide sequence selected from any of 948 sequences (ABZ11119-
XX ABZ12066) or their mature protein coding portion, active domain coding
XX protein or complementary sequences. The polynucleotides are useful for
XX identifying expressed genes or for physical mapping of human genome. The
XX encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight
XX markers, as a food supplement, for generating antibodies, in medical
XX imaging, screening and diagnostic assays and for treating cell-
XX proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
XX or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
XX diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
XX platelet or coagulation disorders, wound, burns, incision, ulcers, liver
XX or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
XX arthritis, etc. Note: The sequence data for this patent did not form part
XX of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 257 AA;
XX
XX Query Match 93.3%; Score 1064; DB 5; Length 257;
XX Best Local Similarity 95.0%; Pred. No. 2e-63;
XX Matches 208; Conservative 0; Mismatches 1; Indels 10; Gaps 1;
QY 1 IVGGRARPHAWPFMVSLQLRGCHFCGATLIAPNFVMSAAHCYANNVAVRVVLGAHNL 60
Db 30 IVGGRARPHAWPFMVSLQLRGCHFCGATLIAPNFVMSAAHCYANNVAVRVVLGAHNL 89
QY 61 SRREPTQVFAVQRIFFENGCTDPVNLNDIVILQLNGSATINANVQVQALPAQGRRLGNGV 120
Db 90 SRREPTQVFAVQRIFFENGCTDPVNLNDIVILQLNGSATINANVQVQALPAQGRRLGNGV 149
```

Db	89	RRQERTQTFESVQRIENFGFDPSSLNDIVIIQLNGSATINANVOVAQLPAQGGVGDRT	148
QY	121	QCLAMGWLLGRNRGIASVLOELNVTVVTSLSLRRSNVCTLVNRGQAGVCFGDSGSLVCN	179
Db	149	QCLAMGWLLGRNRGIASVLOELNVTVVTSLSLRRSNVCTLVNRGQAGVCFGDSGSLVCN	208
QY	180	GLIHGIASFVRGGCAGSLYPDAFAPVAQFVNWIDSIIQR	218
Db	209	NNLVQGGIDSFIRGGCGSLYPDAFAPVAEPADWINSIIR	247
RESULT 10			
AAW08269	ID	AAW08269 standard; protein; 265 AA.	
XX	AC	AAW08269;	
XX	DT	27-AUG-2003 (revised)	
DT	07-MAR-1991	(first entry)	
XX	DE	Mouse serine protease precursor, deduced from the DNA.	
XX	KW	Leukaemia elastase; pulmonary emphysema; rheumatoid arthritis; psoriasis;	
KW	KW	Behcet disease; adult respiratory distress syndrome.	
XX	OS	Mus musculus.	
XX	XX		
XX	XX	Key Location/Qualifiers	
FT	Protein	29..265	
FT		/label= serine protease.	
XX	XX	JP02268680-A.	
PN	XX	02-NOV-1990.	
XX	XX	07-APR-1989; 89JP-00088798.	
XX	XX	07-APR-1989; 89JP-00088798.	
XX	XX	(TORA) TORAY IND INC.	
XX	XX	WPI; 1990-372006/50.	
XX	XX	N-PSDB; AAQ06870.	
XX	XX	Mouse model system - comprises mouse serine protease which shows	
XX	XX	biological activity by polypeptide.	
XX	XX	Claim 2; Page 1; 6pp; Japanese.	
XX	XX	A mouse model system involving the serine protease can be used to	
XX	XX	investigate the role of leukaemia elastase in the development or	
XX	XX	exacerbation of diseases such as pulmonary emphysema, rheumatoid	
XX	XX	arthritis etc. (Updated on 27-AUG-2003 to correct OS field.)	
XX	XX	Sequence 265 AA;	
SQ	Query Match 76.5%; Score 872.5; DB 2; Length 265;		
Best Local Similarity 76.3%; Pred. No. 1.2e-50;			
Matches 167; Conservative 20; Mismatches 31; Indels 1; Gaps 1;			
QY	1	IVGGRARPHAWPFMVSLQRRGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	60
Db	29	IVGGRARPHAWPFMVSLQRRGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	88
QY	61	SRREPTQVFAVQRIENFGTDPNVNLNDIVIIQLNGSATINANVOVAQLPAQGRRLNGV	120
Db	89	RRQERTQTFESVQRIENFGFDPSSLNDIVIIQLNGSATINANVOVAQLPAQGGVGDRT	148
QY	121	QCLAMGWLLGRNRGIASVLOELNVTVVTSLSLRRSNVCTLVNRGQAGVCFGDSGSLVCN	179
Db	149	QCLAMGWLLGRNRGIASVLOELNVTVVTSLSLRRSNVCTLVNRGQAGVCFGDSGSLVCN	208

QY 180 NGLIHGIAFVRCGCGSLYPDAFAPVAQFVNWIDSIQ 218
 Db 209 NNLVQIGDSFIRGCGSLYPDAFAPVAEFADINSIIR 247

RESULT 11

AAR85639
 ID AAR85639 standard; protein; 256 AA.

XX AAR85639;
 DT 23-APR-1996 (first entry)
 XX MY17 preproPR-3.
 KW PR-3; preproPR-3; MY17; human neutrophil protease-3; serine protease;
 KW tumour necrosis factor alpha; TNFalpha; HL60; MY17; B cell; T cell;
 KW tumour necrosis factor alpha convertase; cytokine; septic shock;
 KW rheumatoid arthritis; cachexia; cerebral malaria; graft-host disease;
 KW ischaemia/reperfusion injury; autoimmune disease; AIDS.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..25 /note= "leader sequence present only in preproPR-3"
 FT Peptide 26..27 /note= "dipeptide present in proPR-3"
 FT Protein 28..256 /note= "mature PR-3"

XX W09524501-AL.

XX 14-SRP-1995.

XX 02-MAR-1995; 95WO-US002513.

XX 07-MAR-1994; 94US-00208574.

PR 19-APR-1994; 94US-00230428.

PR 27-FEB-1995; 95US-00394600.

PR 28-FEB-1995; 95US-00395456.

XX (CETU) CETUS ONCOLOGY CORP.

XX Halenbeck RF, Kriegler M, Perez C, Jewell DA, Kothe KE;

XX WPI; 1995-328287/42.

DR N-PSDB; AAT02565.

XX Identification of inhibitors of mature TNFalpha prodn. - useful for
 treatment of septic shock, rheumatoid arthritis, etc.

XX Example 2; Page 82; 96pp; English.

XX This sequence represents the preproPR-3. PR-3 is active recombinant human
 CC neutrophil protease-3. PR-3 is a serine protease, and is a tumour
 CC necrosis factor alpha (TNFalpha) convertase. The cDNA encoding this
 CC sequence was isolated from the HL60 cell clone MY17. The mature PR-3 can
 CC be used in the method of the invention for identifying agents that
 CC inhibit cleavage of proTNFalpha to mature TNFalpha. In the method,
 CC proTNFalpha is incubated with PR-3 (or another TNFalpha convertase), and
 CC the cleavage of the proTNFalpha is measured by a colourimetric assay.
 CC This is then repeated in the presence of a test compound that is thought
 CC to inhibit this process. The results of the two reactions are then
 CC compared to determine whether the test compound is an inhibitor. The
 CC cleavage inhibitors can be used in the treatment of septic shock.
 CC rheumatoid arthritis, cachexia, cerebral malaria, ischaemia/reperfusion
 CC injury, graft-host disease, autoimmune diseases, and AIDS. PR-3 can be
 CC used to treat unwanted B cell/T cell interaction by contacting it with T
 CC cells to cause the release of membrane-bound cytokines

XX Sequence 256 AA;

Query Match 56.1%; Score 639.5; DB 2; Length 256;
 Best Local Similarity 54.5%; Pred. No. 3.9e-35;
 Matches 121; Conservative 40; Mismatches 58; Indels 3; Gaps 1;

QY 1 IVGRRRAPHWPFVMSLQLR--GSHFCGATLIAPNFVMSAAHCVANVNVRAVRVVLGA 57
 Db 28 IVGGHEAQHSRPYMASLQMRGNPGSHFCGTLIHPFVLTAAHCLRDIPQLRVNVVLGA 87
 QY 58 HNLSRREPTQVAFQVIFENGCTDPVNLNDIVILQLNGSATINANVQVLAQGRRLG 117
 Db 88 HNVRTQEPHQHFSVAQVFLNNYDAENKLDILLQLSSPANLSASVATVQLPQQDQPPV 147
 QY 118 NGVQCLAMGWLGLGRNGIASVLQELNVTVTSLCRSNVCTLVRCRQACVCEGDSGSL 177
 Db 148 HGTQCLAMGWRGVGAHDPPAQVQLBLNVTVTFPCRPHNICTFVPRKAGICFGDGGG 207
 QY 178 VCNGLIHGIAFVRCGCGSLYPDAFAPVAQFVNWIDSIQ 219
 Db 208 ICDGIIQIGDSFVWGCATRLFPDFTRVALYVDWIRSLRR 249

RESULT 12

ABW02656

ID ABW02656 standard; protein; 256 AA.

XX AC ABW02656;

DT 11-MAR-2004 (first entry)

DE Human preproPR-3 protein from MY17 clone.

KW Human; tumour necrosis factor alpha; neutrophil protease; PR-3; P-29b;
 KW serine protease; proteinase-3; myeloblastin; Wegener's granulomatosis;
 KW rheumatoid arthritis; acquired immune deficiency syndrome; cachexia;
 KW TNFalpha convertase; sepsis; therapy; autoimmune disease; AIDS; enzyme.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..25 /note= "PR-3 leader peptide"

FT Peptide 26..27 /note= "proPR-3 peptide"

FT Protein 28..256 /note= "Human mature PR-3 protein"

XX US6599706-B1.

XX 29-JUL-2003.

XX 07-JUN-1995; 95US-00487453.

PR 16-AUG-1989; 89US-00395253.

PR 07-MAR-1994; 94US-00208574.

PR 14-APR-1994; 94US-00230428.

PR 27-FEB-1995; 95US-00394600.

PR 28-FEB-1995; 95US-00395456.

XX (CHIR) CHIRON CORP.

XX Halenbeck RF, Kriegler M, Tuttleman J, Perez C, Jewell DA;

PI Kothe KE;

XX WPI; 2003-851193/79.

DR N-PSDB; AAD64612.

XX Determination of presence of inhibitor human-neutrophil protease by,
 PT contacting recombinant mature human-neutrophil protease specified
 PT sequence of amino acids, with sample having inhibitor of human-neutrophil
 PT protease.

XX Claim 1; SEQ ID NO 23; Opp; English.

contacting recombinant mature human-neutrophil protease having specified sequence of amino acids, with sample having inhibitor of human-neutrophil protease.

Disclosure; SEQ ID NO 20; Opp; English.

The invention relates to TNFalpha (tumour necrosis factor alpha) convertase, a human-neutrophil protease (PR-3) capable of converting pro-TNFalpha to mature TNFalpha. PR-3 (serine protease) is also referred to as proteinase-3, P-29b and myeloblastin. The invention specifically relates to the identification of compositions and methods for identifying inhibitors of TNFalpha convertase. Inhibitors of the invention are used for determining Wegener's granulomatosis and for treating diseases associated with elevated levels of hormones particularly sepsis, rheumatoid arthritis, cachexia, acquired immune deficiency syndrome (AIDS) and autoimmune diseases. The present sequence is human mature PR-3 protein

Query Match 56.0%; Score 638.5; DB 7; Length 229;
Best Local Similarity 54.1%; Pred. No. 4.1e-35;
Matches 120; Conservative 41; Mismatches 58; Indels 3; Gaps 1;

1 IVGRRARPHAMPFVMSLQLR---GGHFCGATLIAPNFVMSAAHCVANVVRVVLGA 57
28 IVGGHEAQPHSRPYMASLQMRGNFSGHFCGGTLIHPFVLTAACHLURDIQRLVNVVLGA 87
58 HNLSSRREPTQVFAVORIFENGTDVNLNDIVILQNGSATINANVQVAPQAGRRLG 117
88 HNVRTQPTQOHFSVAQVFLNNYDAENKLDLILQLSSPANLSASVATVQLPQDDQVPV 147
118 NGVQCLAMGWLGLGRNKGIAVLQELNVTVTSICRRSNVCTLVGRQAGVCFGDSGPL 177
148 HGTQCLAMGWRGVGAHDPQAQVQLQELNVTVTFFCRPHNICTFVPRKAGICFGDSGGPL 207
178 VCNGLIHGIAFVRGCGCAGLYPDAPAFVPAQVFNWIDSIIOR 219
208 ICDGIIQIGDSFVIWGCATRLFPDFFTRVALYVDWIRSTLRR 249

RESULT 14
AAR45403
ID AAR45403 standard; protein; 256 AA.
XX
AC AAR45403;
XX AC
XX 25-MAR-2003 (revised)
DT 18-JUL-1994 (first entry)
XX
XX Deduced sequence of human proteinase-3 (PR-3).
XX TNF convertase; proteinase-3; PR-3; tumour necrosis factor; proTNF.
XX Homo sapiens.
XX OS
XX WO9400555-A2.
XX
XX 06-JAN-1994.
XX
XX 25-JUN-1993; 93WO-US006120.
XX
XX 25-JUN-1992; 92US-00905546.
XX
XX (CETU) CETUS ONCOLOGY CORP.
XX
XX Kriegler M, Perez C, Halenbeck RF, Jewell DA, Koths KE;
XX WPI; 1994-026195/03.
XX N-PSDB; AAQ54498.
XX
XX Cpd. which inhibit formation of mature tumour necrosis factor from its precursor - identified using TNF convertase, e.g. mutein(s), antibodies

The invention relates to TNFalpha (tumour necrosis factor alpha) convertase, a human-neutrophil protease (PR-3) capable of converting pro-TNFalpha to mature TNFalpha. PR-3 (serine protease) is also referred to as proteinase-3, P-29b and myeloblastin. The invention specifically relates to the identification of compositions and methods for identifying inhibitors of TNFalpha convertase. Inhibitors of the invention are used for determining Wegener's granulomatosis and for treating diseases associated with elevated levels of hormones particularly sepsis, rheumatoid arthritis, cachexia, acquired immune deficiency syndrome (AIDS) and autoimmune diseases. The present sequence is human preproPR-3 protein

Query Match 56.1%; Score 639.5; DB 7; Length 256;
Best Local Similarity 54.5%; Pred. No. 3.9e-35;
Matches 121; Conservative 40; Mismatches 58; Indels 3; Gaps 1;

1 IVGRRARPHAMPFVMSLQLR---GGHFCGATLIAPNFVMSAAHCVANVVRVVLGA 57
28 IVGGHEAQPHSRPYMASLQMRGNFSGHFCGGTLIHPFVLTAACHLURDIQRLVNVVLGA 87
58 HNLSSRREPTQVFAVORIFENGTDVNLNDIVILQNGSATINANVQVAPQAGRRLG 117
88 HNVRTQPTQOHFSVAQVFLNNYDAENKLDLILQLSSPANLSASVATVQLPQDDQVPV 147
118 NGVQCLAMGWLGLGRNKGIAVLQELNVTVTSICRRSNVCTLVGRQAGVCFGDSGPL 177
148 HGTQCLAMGWRGVGAHDPQAQVQLQELNVTVTFFCRPHNICTFVPRKAGICFGDSGGPL 207
178 VCNGLIHGIAFVRGCGCAGLYPDAPAFVPAQVFNWIDSIIOR 219
208 ICDGIIQIGDSFVIWGCATRLFPDFFTRVALYVDWIRSTLRR 249

RESULT 13
ABW02654
ID ABW02654 standard; protein; 229 AA.
XX
AC ABW02654;
XX
XX 11-MAR-2004 (first entry)
XX
XX Human mature PR-3 protein.
XX
XX Human; tumour necrosis factor alpha; neutrophil protease; PR-3; P-29b;
XX serine protease; proteinase-3; myeloblastin; Wegener's granulomatosis;
XX rheumatoid arthritis; acquired immune deficiency syndrome; cachexia;
XX TNFalpha convertase; sepsis; therapy; autoimmune disease; AIDS; enzyme.
XX
XX Homo sapiens.
XX
XX US6599706-B1.
XX
XX 29-JUL-2003.
XX
XX 07-JUN-1995; 95US-00487453.
XX
XX 16-AUG-1989; 89US-00395253.
XX 07-MAR-1994; 94US-00208574.
XX 14-APR-1994; 94US-00230428.
XX 27-FEB-1995; 95US-00394600.
XX 28-FEB-1995; 95US-00395456.
XX
XX (CHIR) CHIRON CORP.
XX
XX Halenbeck RF, Kriegler M, Tuttleman J, Perez C, Jewell DA;
XX Koths KE;
XX
XX WPI; 2003-851193/79.
XX N-PSDB; AAD64602.
XX
XX Determination of presence of inhibitor human-neutrophil protease by,

PT or peptide phosphonate(s), for preventing and treating sepsis, AIDS, auto
 XX -immune disease etc.

PS Disclosure; Fig 2; 69pp; English.

XX
 CC PROTNP refers to TNF having a molecular weight of about 26,000, which is
 CC the prohormone form of TNF α . PROTNF is cleaved to a lower molecular
 CC weight 'mature' form, pref. 17kd, which, in its multimeric (usually
 CC trimetric) form, is substantially involved in producing life- threatening
 CC physiological changes associated with sepsis. PROTNF is cleaved by
 CC convertase. One TNF convertase is serine protease proteinase-3, also
 CC called PR-3, P-29b or myeloblastin. A suitable source of convertase is the
 CC HL60 cell line (or extracts, or the culture media in which it is grown).
 CC The convertase produced by HL60 has been sequenced and is identical to
 CC the known lymphocyte serine protease PR-3 which has other activities
 CC unrelated to TNF processing. (Updated on 25-MAR-2003 to correct PN
 CC field.)

XX Sequence 256 AA;

SQ Query Match 56.0%; Score 638.5; DB 2; Length 256;
 Best Local Similarity 54.1%; Pred. No. 4.5e-35;
 Matches 120; Conservative 41; Mismatches 58; Indels 3; Gaps 1;

QY 1 IVGGRRARPHAWPFMVSLQLR---GGHFCGATLIAPNFVMSAAHCVANVNVRAVRVVLGA 57
 DB 28 IVGGHEAQPHSRPYMASLQMRGNPGSHFCGGTLIHPSFVLTAACHCLRDIPQRLVNVVLGA 87
 QY 58 HNLSRREPTQVFAVQRIPENGTDPVNLNDIVILQNGSATINANVQVAQLPAQGRRLG 117
 DB 88 HNVRTQETQOHFSVAQVFLNNYDAENKLDVLLIQSSPANLSASVATVQLPQQQPPV 147
 QY 118 NGVQCLAMGWLGRNRIASVLQELNVTVTSLCRSRNVCTLVRCRQAGVCFDGSGL 177
 DB 148 HGTQCLAMGWGRVGAHDPPAQVLQELNVTVTFFCRPHNICTFVPRKAGICFGDSGGL 207
 QY 178 VCNGLTHGIASFVGGCAGSLYPDAFAPVAQFVNWIDSIQR 219
 DB 208 ICDGIIQIGDSFVINGCATRLFPDPFTRVALYVDWIRSLRR 249

RESULT 15

ABW02646
 ID ABW02646 standard; protein; 256 AA.

XX AC ABW02646;

XX 11-MAR-2004 (first entry)

XX Human preproPR-3 protein.

XX Human; tumour necrosis factor alpha; neutrophil protease; PR-3; P-29b;
 KW serine protease; proteinase-3; myeloblastin; Wegener's granulomatosis;
 KW rheumatoid arthritis; acquired immune deficiency syndrome; cachexia;
 KW TNFalpha convertase; sepsis; therapy; autoimmune disease; AIDS; enzyme.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..25 /note= "PR-3 leader peptide"

FT Peptide 26..27 /note= "proPR-3 peptide"

FT Protein 28..256 /note= "Human mature PR-3 protein"

XX US6599706-B1.

XX 29-JUL-2003.

XX 07-JUN-1995; 95US-00487453.

XX 16-AUG-1989; 89US-00395253.

PR 07-MAR-1994; 94US-00208574.
 PR 14-APR-1994; 94US-00230428.
 PR 27-FEB-1995; 95US-00394600.
 PR 28-FEB-1995; 95US-00395456.

XX (CHIR) CHIRON CORP.

XX Halenbeck RP, Kriegler M, Tuttleman J, Perez C, Jewell DA;
 PI Koths KE;

XX WPI: 2003-851193/79.

DR N-PSDB; AAD64602.

XX Determination of presence of inhibitor human-neutrophil protease by,
 PT contacting recombinant mature human-neutrophil protease having specified
 PT sequence of amino acids, with sample having inhibitor of human-neutrophil
 PT protease.

XX Disclosure; Col 49-52; Opp; English.

XX The invention relates to TNFalpha (tumour necrosis factor alpha)
 CC convertase, a human-neutrophil protease (PR-3) capable of converting pro-
 CC TNFalpha to mature TNFalpha. PR-3 (serine protease) is also referred to
 CC as proteinase-3, P-29b and myeloblastin. The invention specifically
 CC relates to the identification of compositions and methods for identifying
 CC inhibitors of TNFalpha convertase. Inhibitors of the invention are used
 CC for determining Wegener's granulomatosis and for treating diseases
 CC associated with elevated levels of hormones particularly sepsis,
 CC rheumatoid arthritis, cachexia, acquired immune deficiency syndrome
 CC (AIDS) and autoimmune diseases. The present sequence is human preproPR-3
 CC protein

XX Sequence 256 AA;

SQ Query Match 56.0%; Score 638.5; DB 7; Length 256;
 Best Local Similarity 54.1%; Pred. No. 4.5e-35;
 Matches 120; Conservative 41; Mismatches 58; Indels 3; Gaps 1;

QY 1 IVGGRRARPHAWPFMVSLQLR---GGHFCGATLIAPNFVMSAAHCVANVNVRAVRVVLGA 57

DB 28 IVGGHEAQPHSRPYMASLQMRGNPGSHFCGGTLIHPSFVLTAACHCLRDIPQRLVNVVLGA 87

QY 58 HNLSRREPTQVFAVQRIPENGTDPVNLNDIVILQNGSATINANVQVAQLPAQGRRLG 117

DB 88 HNVRTQETQOHFSVAQVFLNNYDAENKLDVLLIQSSPANLSASVATVQLPQQQPPV 147

QY 118 NGVQCLAMGWLGRNRIASVLQELNVTVTSLCRSRNVCTLVRCRQAGVCFDGSGL 177

DB 148 HGTQCLAMGWGRVGAHDPPAQVLQELNVTVTFFCRPHNICTFVPRKAGICFGDSGGL 207

QY 178 VCNGLTHGIASFVGGCAGSLYPDAFAPVAQFVNWIDSIQR 219

DB 208 ICDGIIQIGDSFVINGCATRLFPDPFTRVALYVDWIRSLRR 249

Search completed: April 18, 2005, 12:46:20
 Job time : 176 secs

THIS PAGE BLANK (USPTO)